

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 3, 2004, 06:21:53 ; Search time 105 Seconds  
(without alignments)  
78.128 Million cell updates/sec

Title: US-09-733-239-1  
Perfect score: 139  
Sequence: 1 RILAVERYLKDQQLLGWCSGKLIC 26

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2672

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%  
Maximum Match 100%  
Listing first 500 summaries

Database : SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	139	100.0	117	15	Q9YYZ9 human immun
2	139	100.0	117	15	Q9YRU1 human immun
3	139	100.0	122	15	Q9QIU3 human immun
4	139	100.0	122	15	Q9EA97 human immun
5	139	100.0	122	15	Q9WQZ3 human immun
6	139	100.0	122	15	Q9YXP4 human immun
7	139	100.0	122	15	Q7ZJR4 human immun
8	139	100.0	123	15	Q8AEX2 human immun
9	139	100.0	144	15	Q7ZCD7 human immun
10	139	100.0	144	15	Q7ZCD6 human immun
11	139	100.0	145	15	Q7ZC52 human immun
12	139	100.0	145	15	Q7ZC48 human immun
13	139	100.0	155	15	Q8J3N1 human immun
14	139	100.0	357	15	Q78119 human immun
15	139	100.0	358	15	Q78120 human immun
16	139	100.0	588	15	Q993A8 human immun

17	139	100.0	588	15	Q993A7	Q993a7 human immun
18	139	100.0	589	15	Q993B1	Q993b1 human immun
19	139	100.0	590	15	Q993A9	Q993a9 human immun
20	139	100.0	616	15	Q993B0	Q993b0 human immun
21	139	100.0	618	15	Q993B2	Q993b2 human immun
22	139	100.0	727	15	Q9Q723	Q9q723 human immun
23	139	100.0	747	15	Q70607	Q70607 human immun
24	139	100.0	748	15	Q70606	Q70606 human immun
25	139	100.0	752	15	Q70604	Q70604 human immun
26	139	100.0	752	15	Q70605	Q70605 human immun
27	139	100.0	752	15	Q70608	Q70608 human immun
28	139	100.0	757	15	Q9Q722	Q9q722 human immun
29	139	100.0	800	15	Q9WMV1	Q9wmv1 human immun
30	139	100.0	801	15	Q9WMU9	Q9wmu9 human immun
31	139	100.0	807	15	Q8Q2X2	Q8q2x2 human immun
32	139	100.0	809	15	Q9WMV0	Q9wmv0 human immun
33	139	100.0	826	15	Q9DVL1	Q9dvl1 human immun
34	139	100.0	845	15	Q9ID89	Q9id89 human immun
35	139	100.0	847	15	Q69996	Q69996 human immun
36	139	100.0	849	15	Q9YKT7	Q9ykt7 human immun
37	139	100.0	849	15	Q90CI9	Q90ci9 human immun
38	139	100.0	849	15	Q9YKT4	Q9ykt4 human immun
39	139	100.0	850	15	Q9QBY2	Q9qby2 human immun
40	139	100.0	851	15	Q9QBZ4	Q9qbz4 human immun
41	139	100.0	854	15	Q56566	Q56566 human immun
42	139	100.0	854	15	Q85582	Q85582 human immun
43	139	100.0	854	15	Q8UNL0	Q8unl0 human immun
44	139	100.0	854	15	Q72502	Q72502 human immun
45	139	100.0	854	15	Q90178	Q90178 human immun
46	139	100.0	854	15	Q9DVL2	Q9dvl2 human immun
47	139	100.0	854	15	Q78705	Q78705 human immun
48	139	100.0	855	15	Q8AQV7	Q8aqv7 human immun
49	139	100.0	856	15	Q74090	Q74090 human immun
50	139	100.0	856	15	Q92877	Q92877 simian-huma
51	139	100.0	856	15	Q74599	Q74599 human immun
52	139	100.0	857	15	Q92822	Q92822 human immun
53	139	100.0	857	15	Q71013	Q71013 human immun
54	139	100.0	857	15	Q89654	Q89654 human immun
55	139	100.0	857	15	Q92823	Q92823 human immun
56	139	100.0	857	15	Q9QBZ0	Q9qbz0 human immun
57	139	100.0	859	15	Q9YUZ4	Q9yuz4 human immun
58	139	100.0	859	15	Q9WLJ1	Q9wlj1 human immun
59	139	100.0	860	15	Q7SQA7	Q7sqa7 human immun
60	139	100.0	862	15	Q8UNL9	Q8unl9 human immun
61	139	100.0	862	15	Q7SQA2	Q7sqa2 human immun
62	139	100.0	864	15	Q9YP39	Q9yp39 human immun
63	139	100.0	864	15	Q7ZJC8	Q7zjc8 human immun
64	139	100.0	866	15	Q9WPZ4	Q9wpz4 human immun
65	139	100.0	868	15	Q8ADN9	Q8adn9 human immun
66	139	100.0	870	15	Q8Q2X1	Q8q2x1 human immun
67	139	100.0	870	15	Q8Q2X0	Q8q2x0 human immun
68	138	99.3	94	15	Q8AEX3	Q8aex3 human immun
69	138	99.3	109	15	Q40239	Q40239 human immun
70	138	99.3	112	15	Q8UQW2	Q8uqw2 human immun
71	138	99.3	117	15	Q9QQN5	Q9qqn5 human immun
72	138	99.3	117	15	Q9YRT2	Q9yrt2 human immun
73	138	99.3	117	15	Q9YRS4	Q9yrs4 human immun
74	138	99.3	117	15	Q9QQN0	Q9qqn0 human immun
75	138	99.3	117	15	Q9YZ04	Q9yz04 human immun
76	138	99.3	117	15	Q9YRS6	Q9yrs6 human immun
77	138	99.3	117	15	Q9WKU0	Q9wku0 human immun
78	138	99.3	117	15	Q9WM72	Q9wm72 human immun
79	138	99.3	117	15	Q9QQN3	Q9qqn3 human immun
80	138	99.3	117	15	Q9YZ01	Q9yz01 human immun
81	138	99.3	117	15	Q9YRS2	Q9yrs2 human immun
82	138	99.3	117	15	Q9YYZ2	Q9yyz2 human immun
83	138	99.3	117	15	Q7SVI8	Q7svi8 human immun
84	138	99.3	117	15	Q7SVI4	Q7svi4 human immun
85	138	99.3	117	15	Q7SVG4	Q7svg4 human immun
86	138	99.3	117	15	Q7SVG1	Q7svg1 human immun
87	138	99.3	117	15	Q7SVF9	Q7svf9 human immun
88	138	99.3	117	15	Q7SVF7	Q7svf7 human immun
89	138	99.3	117	15	Q7SVF4	Q7svf4 human immun

90	138	99.3	117	15	Q7SVF3	Q7svf3	human	immun	163	138	99.3	122	15	Q9IJN6	Q9ijn6	human	immun
91	138	99.3	117	15	Q7SVF2	Q7svf2	human	immun	164	138	99.3	122	15	Q90DR2	Q90dr2	human	immun
92	138	99.3	117	15	Q7SVE8	Q7sve8	human	immun	165	138	99.3	122	15	Q90DP8	Q90dp8	human	immun
93	138	99.3	117	15	Q7SVE7	Q7sve7	human	immun	166	138	99.3	122	15	Q9ILJ6	Q9ilj6	human	immun
94	138	99.3	117	15	Q7SVE4	Q7sve4	human	immun	167	138	99.3	122	15	Q9IJP6	Q9ijp6	human	immun
95	138	99.3	118	15	Q9ESR0	Q9esr0	human	immun	168	138	99.3	122	15	Q9EA88	Q9ea88	human	immun
96	138	99.3	121	15	Q90DJ5	Q90dj5	human	immun	169	138	99.3	122	15	Q90DS1	Q90ds1	human	immun
97	138	99.3	122	15	Q9EA94	Q9ea94	human	immun	170	138	99.3	122	15	Q9IJQ6	Q9ijq6	human	immun
98	138	99.3	122	15	Q90DJ2	Q90dj2	human	immun	171	138	99.3	122	15	Q9IJQ5	Q9ijq5	human	immun
99	138	99.3	122	15	Q9IJN0	Q9ijn0	human	immun	172	138	99.3	122	15	Q90DK2	Q90dk2	human	immun
100	138	99.3	122	15	Q9EA85	Q9ea85	human	immun	173	138	99.3	122	15	Q90DN1	Q90dn1	human	immun
101	138	99.3	122	15	Q9QIW8	Q9qiw8	human	immun	174	138	99.3	122	15	Q90DM2	Q90dm2	human	immun
102	138	99.3	122	15	Q9QIW1	Q9qiw1	human	immun	175	138	99.3	122	15	Q90DN3	Q90dn3	human	immun
103	138	99.3	122	15	Q9EA81	Q9ea81	human	immun	176	138	99.3	122	15	Q9IJP2	Q9ijp2	human	immun
104	138	99.3	122	15	Q9YXQ0	Q9yxq0	human	immun	177	138	99.3	122	15	Q90DS7	Q90ds7	human	immun
105	138	99.3	122	15	Q9EAA4	Q9eaa4	human	immun	178	138	99.3	122	15	Q9QIU7	Q9qiu7	human	immun
106	138	99.3	122	15	Q9QIW0	Q9qiw0	human	immun	179	138	99.3	122	15	Q9IJQ1	Q9ijq1	human	immun
107	138	99.3	122	15	Q90DQ9	Q90dq9	human	immun	180	138	99.3	122	15	Q9WR01	Q9wr01	human	immun
108	138	99.3	122	15	Q9IJN1	Q9ijn1	human	immun	181	138	99.3	122	15	Q9IJL1	Q9ijl1	human	immun
109	138	99.3	122	15	Q90DK8	Q90dk8	human	immun	182	138	99.3	122	15	Q9IJM9	Q9ijm9	human	immun
110	138	99.3	122	15	Q90DS5	Q90ds5	human	immun	183	138	99.3	122	15	Q9IJQ9	Q9ijq9	human	immun
111	138	99.3	122	15	Q90DQ4	Q90dq4	human	immun	184	138	99.3	122	15	Q9IJP5	Q9ijp5	human	immun
112	138	99.3	122	15	Q9EAA5	Q9eaa5	human	immun	185	138	99.3	122	15	Q9ILM2	Q9ilm2	human	immun
113	138	99.3	122	15	Q9IJM8	Q9ijm8	human	immun	186	138	99.3	122	15	Q90DT2	Q90dt2	human	immun
114	138	99.3	122	15	Q9EAA2	Q9eaa2	human	immun	187	138	99.3	122	15	Q9YXP3	Q9yxp3	human	immun
115	138	99.3	122	15	Q90DL1	Q90dl1	human	immun	188	138	99.3	122	15	Q9EA82	Q9ea82	human	immun
116	138	99.3	122	15	Q90DS4	Q90ds4	human	immun	189	138	99.3	122	15	Q90DK7	Q90dk7	human	immun
117	138	99.3	122	15	Q9QIW3	Q9qiw3	human	immun	190	138	99.3	122	15	Q9IJQ4	Q9ijq4	human	immun
118	138	99.3	122	15	Q90PX7	Q90px7	human	immun	191	138	99.3	122	15	Q90DM3	Q90dm3	human	immun
119	138	99.3	122	15	Q9QIV8	Q9qiv8	human	immun	192	138	99.3	122	15	Q90DL6	Q90dl6	human	immun
120	138	99.3	122	15	Q9WQZ1	Q9wqz1	human	immun	193	138	99.3	122	15	Q9WQZ4	Q9wqz4	human	immun
121	138	99.3	122	15	Q90PY1	Q90py1	human	immun	194	138	99.3	122	15	Q9YXN5	Q9yxn5	human	immun
122	138	99.3	122	15	Q9ILL3	Q9ill3	human	immun	195	138	99.3	122	15	Q9QIU8	Q9qiu8	human	immun
123	138	99.3	122	15	Q90DN6	Q90dn6	human	immun	196	138	99.3	122	15	Q90DN8	Q90dn8	human	immun
124	138	99.3	122	15	Q9QIV7	Q9qiv7	human	immun	197	138	99.3	122	15	Q90DN5	Q90dn5	human	immun
125	138	99.3	122	15	Q90DP5	Q90dp5	human	immun	198	138	99.3	122	15	Q9IJP7	Q9ijp7	human	immun
126	138	99.3	122	15	Q90DT0	Q90dt0	human	immun	199	138	99.3	122	15	Q90DL2	Q90dl2	human	immun
127	138	99.3	122	15	Q9IJK5	Q9ijk5	human	immun	200	138	99.3	122	15	Q7ZJS6	Q7zjs6	human	immun
128	138	99.3	122	15	Q9YXN7	Q9yxn7	human	immun	201	138	99.3	122	15	Q7ZJS2	Q7zjs2	human	immun
129	138	99.3	122	15	Q90DP0	Q90dp0	human	immun	202	138	99.3	122	15	Q7ZJS1	Q7zjs1	human	immun
130	138	99.3	122	15	Q9WQZ7	Q9wqz7	human	immun	203	138	99.3	122	15	Q7ZJS0	Q7zjs0	human	immun
131	138	99.3	122	15	Q90DQ7	Q90dq7	human	immun	204	138	99.3	122	15	Q7ZJR8	Q7zjr8	human	immun
132	138	99.3	122	15	Q9IILK4	Q9ilk4	human	immun	205	138	99.3	122	15	Q7ZJR7	Q7zjr7	human	immun
133	138	99.3	122	15	Q9YXN4	Q9yxn4	human	immun	206	138	99.3	122	15	Q7ZJR6	Q7zjr6	human	immun
134	138	99.3	122	15	Q9QIW7	Q9qiw7	human	immun	207	138	99.3	122	15	Q7ZJR5	Q7zjr5	human	immun
135	138	99.3	122	15	Q9EA84	Q9ea84	human	immun	208	138	99.3	122	15	Q7ZJP0	Q7zjp0	human	immun
136	138	99.3	122	15	Q9IJQ8	Q9ijq8	human	immun	209	138	99.3	123	15	Q8J3S3	Q8j3s3	human	immun
137	138	99.3	122	15	Q9YXR0	Q9yxr0	human	immun	210	138	99.3	123	15	Q8J3R5	Q8j3r5	human	immun
138	138	99.3	122	15	Q90DN0	Q90dn0	human	immun	211	138	99.3	123	15	Q9YXR3	Q9yxr3	human	immun
139	138	99.3	122	15	Q9YXQ7	Q9yxq7	human	immun	212	138	99.3	123	15	Q8J3S2	Q8j3s2	human	immun
140	138	99.3	122	15	Q9YXP9	Q9yxp9	human	immun	213	138	99.3	123	15	Q8AEX1	Q8aex1	human	immun
141	138	99.3	122	15	Q90DI9	Q90di9	human	immun	214	138	99.3	124	15	Q8J3R7	Q8j3r7	human	immun
142	138	99.3	122	15	Q90DN2	Q90dn2	human	immun	215	138	99.3	124	15	Q9YZ03	Q9yz03	human	immun
143	138	99.3	122	15	Q9YXR4	Q9yxr4	human	immun	216	138	99.3	125	15	Q9IWP9	Q9iwp9	human	immun
144	138	99.3	122	15	Q9IJQ7	Q9ijq7	human	immun	217	138	99.3	126	15	Q9IWQ9	Q9iwq9	human	immun
145	138	99.3	122	15	Q9IJL2	Q9ijl2	human	immun	218	138	99.3	127	15	Q9YYX6	Q9yyx6	human	immun
146	138	99.3	122	15	Q90DR7	Q90dr7	human	immun	219	138	99.3	127	15	Q9IWR0	Q9iwr0	human	immun
147	138	99.3	122	15	Q90DR8	Q90dr8	human	immun	220	138	99.3	127	15	Q9WM82	Q9wm82	human	immun
148	138	99.3	122	15	Q9YXQ1	Q9yxq1	human	immun	221	138	99.3	127	15	Q9WM85	Q9wm85	human	immun
149	138	99.3	122	15	Q90DN9	Q90dn9	human	immun	222	138	99.3	127	15	Q9YYW8	Q9yyw8	human	immun
150	138	99.3	122	15	Q9QIV3	Q9qiv3	human	immun	223	138	99.3	128	15	Q9IHY1	Q9ihy1	human	immun
151	138	99.3	122	15	Q9IJL3	Q9ijl3	human	immun	224	138	99.3	129	15	Q9YYZ0	Q9yyz0	human	immun
152	138	99.3	122	15	Q9EA95	Q9ea95	human	immun	225	138	99.3	129	15	Q9YYZ2	Q9yyz2	human	immun
153	138	99.3	122	15	Q90DL7	Q90dl7	human	immun	226	138	99.3	130	15	Q9IWR6	Q9iwr6	human	immun
154	138	99.3	122	15	Q90DQ8	Q90dq8	human	immun	227	138	99.3	130	15	Q9YYW6	Q9yyw6	human	immun
155	138	99.3	122	15	Q90DJ1	Q90dj1	human	immun	228	138	99.3	132	15	Q9IWO0	Q9iwo0	human	immun
156	138	99.3	122	15	Q9YXM8	Q9yxm8	human	immun	229	138	99.3	133	15	Q8UQZ6	Q8uqz6	human	immun
157	138	99.3	122	15	Q90DI8	Q90di8	human	immun	230	138	99.3	133	15	Q8UQW8	Q8uqw8	human	immun
158	138	99.3	122	15	Q9IJN7	Q9ijn7	human	immun	231	138	99.3	133	15	Q9YZ13	Q9yz13	human	immun
159	138	99.3	122	15	Q90DS6	Q90ds6	human	immun	232	138	99.3	133	15	Q90Q18	Q90q18	human	immun
160	138	99.3	122	15	Q90DP3	Q90dp3	human	immun	233	138	99.3	133	15	Q90Q57	Q90q57	human	immun
161	138	99.3	122	15	Q90DK0	Q90dk0	human	immun	234	138	99.3	133	15	Q90Q63	Q90q63	human	immun
162	138	99.3	122	15	Q90DR3	Q90dr3	human	immun	235	138	99.3	133	15	Q90PZ3	Q90pz3	human	immun



382	138	99.3	847	15	Q7ZB25	Q7zbz5 human immun
383	138	99.3	848	15	Q9IV28	Q9iv28 human immun
384	138	99.3	848	15	Q9WC60	Q9wc60 human immun
385	138	99.3	848	15	Q7ZB21	Q7zbz1 human immun
386	138	99.3	849	15	O11944	O11944 human immun
387	138	99.3	849	15	Q9IBN3	Q9ibn3 human immun
388	138	99.3	849	15	Q8Q851	Q8q851 human immun
389	138	99.3	849	15	Q8J9B8	Q8j9b8 human immun
390	138	99.3	849	15	Q7ZJG6	Q7zjg6 human immun
391	138	99.3	849	15	Q8JJDH9	Q8jdh9 human immun
392	138	99.3	850	15	O41591	O41591 human immun
393	138	99.3	850	15	Q9WC69	Q9wc69 human immun
394	138	99.3	850	15	Q70003	Q70003 human immun
395	138	99.3	850	15	O11946	O11946 human immun
396	138	99.3	850	15	Q7SVL4	Q7svl4 human immun
397	138	99.3	851	15	O41641	O41641 human immun
398	138	99.3	851	15	O56110	O56110 human immun
399	138	99.3	851	15	Q8Q852	Q8q852 human immun
400	138	99.3	851	15	Q9QBY6	Q9qby6 human immun
401	138	99.3	851	15	Q8Q853	Q8q853 human immun
402	138	99.3	851	15	O56562	O56562 human immun
403	138	99.3	851	15	Q9Q6U7	Q9q6u7 human immun
404	138	99.3	851	15	Q7ZMI4	Q7zmi4 human immun
405	138	99.3	852	15	O41580	O41580 human immun
406	138	99.3	852	15	Q8UPQ5	Q8upq5 human immun
407	138	99.3	852	15	O8UL54	O8ul54 human immun
408	138	99.3	852	15	Q9Q705	Q9q705 human immun
409	138	99.3	852	15	Q73303	Q73303 human immun
410	138	99.3	852	15	O56567	O56567 human immun
411	138	99.3	852	15	Q7ZB27	Q7zbz7 human immun
412	138	99.3	852	15	Q8JDI3	Q8jdi3 human immun
413	138	99.3	853	15	Q9J022	Q9j022 human immun
414	138	99.3	853	15	Q9YMY8	Q9ymy8 human immun
415	138	99.3	853	15	O56108	O56108 human immun
416	138	99.3	853	15	Q9J023	Q9j023 human immun
417	138	99.3	853	15	Q9WS45	Q9ws45 human immun
418	138	99.3	853	15	Q9WBT5	Q9wbt5 human immun
419	138	99.3	853	15	Q8AF21	Q8af21 human immun
420	138	99.3	853	15	Q7ZJF5	Q7zjf5 human immun
421	138	99.3	853	15	Q8JDL1	Q8jdl1 human immun
422	138	99.3	853	15	Q7SVL6	Q7svl6 human immun
423	138	99.3	853	15	Q7SUR3	Q7sur3 human immun
424	138	99.3	854	15	Q7SUR2	Q7sur2 human immun
425	138	99.3	853	15	Q7SIK0	Q7sik0 human immun
426	138	99.3	854	15	O92875	O92875 human immun
427	138	99.3	854	15	Q8USY7	Q8usy7 human immun
428	138	99.3	854	15	Q73300	Q73300 human immun
429	138	99.3	854	15	Q9YVL4	Q9yv14 human immun
430	138	99.3	854	15	O92762	O92762 human immun
431	138	99.3	854	15	O56112	O56112 human immun
432	138	99.3	854	15	Q9IJZ9	Q9ijz9 human immun
433	138	99.3	854	15	Q8Q7Z0	Q8q7z0 human immun
434	138	99.3	854	15	Q8ACA7	Q8aca7 human immun
435	138	99.3	854	15	Q7SVL3	Q7svl3 human immun
436	138	99.3	854	15	Q9WBT4	Q9wbt4 human immun
437	138	99.3	855	15	Q9EIR7	Q9elr7 human immun
438	138	99.3	855	15	Q902G6	Q902g6 human immun
439	138	99.3	855	15	Q7SVL0	Q7svl0 human immun
440	138	99.3	855	15	Q7SUS7	Q7sus7 human immun
441	138	99.3	855	15	Q7SUS6	Q7sus6 human immun
442	138	99.3	855	15	Q7SUS5	Q7sus5 human immun
443	138	99.3	855	15	Q7SUS4	Q7sus4 human immun
444	138	99.3	855	15	Q7SUS2	Q7sus2 human immun
445	138	99.3	855	15	Q7SUS0	Q7sus0 human immun
446	138	99.3	855	15	Q7SUR9	Q7sur9 human immun
447	138	99.3	855	15	Q7SUR8	Q7sur8 human immun
448	138	99.3	855	15	Q7SUR7	Q7sur7 human immun
449	138	99.3	855	15	Q7SUR6	Q7sur6 human immun
450	138	99.3	855	15	Q7SUR5	Q7sur5 human immun
451	138	99.3	855	15	Q7SUR4	Q7sur4 human immun
452	138	99.3	855	15	Q7SUR1	Q7sur1 human immun
453	138	99.3	855	15	Q7SUR0	Q7sur0 human immun
454	138	99.3	855	15	Q7SI11	Q7sil1 human immun
455	138	99.3	856	15	O92873	O92873 human immun
456	138	99.3	856	15	Q77694	Q77694 human immun
457	138	99.3	856	15	P90115	P90115 human immun
458	138	99.3	856	15	Q902G3	Q902g3 human immun
459	138	99.3	856	15	Q9WLH6	Q9wlh6 human immun
460	138	99.3	856	15	Q73297	Q73297 human immun
461	138	99.3	856	15	Q72993	Q72993 human immun
462	138	99.3	856	15	O90079	O90079 human immun
463	138	99.3	856	15	Q8AD87	Q8ad87 human immun
464	138	99.3	856	15	Q7ZJC0	Q7zjc0 human immun
465	138	99.3	856	15	Q8JDH5	Q8jdh5 human immun
466	138	99.3	857	15	Q8JLA2	Q8ula2 human immun
467	138	99.3	857	15	Q8ULA0	Q8ula0 human immun
468	138	99.3	857	15	Q8JBX7	Q8jbx7 human immun
469	138	99.3	857	15	Q8UL89	Q8ul89 human immun
470	138	99.3	857	15	Q8UPL2	Q8upl2 human immun
471	138	99.3	857	15	Q8AQS1	Q8ags1 human immun
472	138	99.3	857	15	Q7ZJ87	Q7zj87 human immun
473	138	99.3	858	15	O92874	O92874 human immun
474	138	99.3	858	15	Q8Q865	Q8q865 human immun
475	138	99.3	858	15	Q8UL75	Q8ul75 human immun
476	138	99.3	858	15	Q8UL76	Q8ul76 human immun
477	138	99.3	858	15	Q8Q867	Q8q867 human immun
478	138	99.3	858	15	O71974	O71974 human immun
479	138	99.3	858	15	Q73293	Q73293 human immun
480	138	99.3	858	15	Q9PY30	Q9py30 human immun
481	138	99.3	858	15	O56107	O56107 human immun
482	138	99.3	858	15	Q8QDZ4	Q8qdz4 human immun
483	138	99.3	858	15	Q7ZJE6	Q7zje6 human immun
484	138	99.3	858	15	Q7SVL1	Q7svl1 human immun
485	138	99.3	858	15	Q7SUT2	Q7sut2 human immun
486	138	99.3	859	15	Q8Q850	Q8q850 human immun
487	138	99.3	859	15	Q8UPN8	Q8upn8 human immun
488	138	99.3	859	15	Q8UL77	Q8ul77 human immun
489	138	99.3	859	15	Q9Q714	Q9q714 human immun
490	138	99.3	859	15	O92937	O92937 human immun
491	138	99.3	859	15	O11947	O11947 human immun
492	138	99.3	859	15	Q8UL80	Q8ul80 human immun
493	138	99.3	859	15	Q8UL79	Q8ul79 human immun
494	138	99.3	859	15	Q8UL73	Q8ul73 human immun
495	138	99.3	859	15	P87924	P87924 human immun
496	138	99.3	859	15	Q7SUT9	Q7sut9 human immun
497	138	99.3	859	15	Q7SUT8	Q7sut8 human immun
498	138	99.3	859	15	Q7SUT7	Q7sut7 human immun
499	138	99.3	859	15	Q7SUT6	Q7sut6 human immun
500	138	99.3	859	15	Q7SUT4	Q7sut4 human immun

ALIGNMENTS

RESULT 1

Q9YYZ9

ID Q9YYZ9 PRELIMINARY; PRT; 117 AA.

AC Q9YYZ9;

DT 01-MAY-1999 (TrEMBLrel. 10; Created)

DT 01-MAY-1999 (TrEMBLrel. 10; Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24; Last annotation update)

DE Gp41 (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=171.005;

RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,

RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;

RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in Uganda.";

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF006876; AAD01320.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.



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DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13970 MW; 4B0F82FC9AF0756D CRC64;

Query Match 100.0%; Score 139; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 23 RILAVERYLKDQQLGIWGCSGKLIC 48

RESULT 2
Q9YRU1 PRELIMINARY; PRT; 117 AA.
AC Q9YRU1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USCM48;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096324; AAD04399.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13986 MW; 4719FD65B98E42E3 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RILAVERYLKDQQLGIWGCSGKLIC 44

RESULT 3
Q9QIU3 PRELIMINARY; PRT; 122 AA.
AC Q9QIU3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=GP41ERRJ28;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165561; AAF08506.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14817 MW; 8D6099E5D3993205 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RILAVERYLKDQQLGIWGCSGKLIC 44

RESULT 4
Q9EA97 PRELIMINARY; PRT; 122 AA.
AC Q9EA97;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX404;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190955; AAG02317.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14763 MW; B9207B0EBE4213AA CRC64;

Query Match 100.0%; Score 139; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RILAVERYLKDQQLGIWGCSGKLIC 44

RESULT 5
Q9WQZ3 PRELIMINARY; PRT; 122 AA.
AC Q9WQZ3;
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DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GH8;  
RA Pieniazek D., Yang C., Lal R.L.;  
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O  
RT isolates provides an alternate region for subtype determination.";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF113589; AAD42757.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 122  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14703 MW; 09E2E31B37786D34 CRC64;  
Query Match 100.0%; Score 139; DB 15; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWCSGKLIC 26  
Db 19 RILAVERYLKDQQLGIWCSGKLIC 44  
RESULT 6  
Q9YXP4 PRELIMINARY; PRT; 122 AA.  
AC Q9YXP4;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein immunodominant region (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RJ96BRP070;  
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,  
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,  
RA Rayfield M.;  
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF034059; AAC79311.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 122  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14819 MW; E3960B97ED1C08D6 CRC64;  
Query Match 100.0%; Score 139; DB 15; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWCSGKLIC 26  
Db 19 RILAVERYLKDQQLGIWCSGKLIC 44  
Query Match 100.0%; Score 139; DB 15; Length 123;  
Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7  
Q7ZJR4 PRELIMINARY; PRT; 122 AA.  
AC Q7ZJR4;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=US4;  
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;  
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M  
RT (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol  
RT integrase, and env gp41.";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY214095; AAO61815.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 122  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14777 MW; AE2C9F40DF21CCFB CRC64;  
Query Match 100.0%; Score 139; DB 15; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWCSGKLIC 26  
Db 19 RILAVERYLKDQQLGIWCSGKLIC 44  
RESULT 8  
Q8AEX2 PRELIMINARY; PRT; 123 AA.  
AC Q8AEX2;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,  
RA Germano de Sousa J., Canas-Ferreira W.;  
RT "Genetic diversity of HIV-1 spreading among intravenous drug users in  
RT Lisbon, Portugal.";  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ429041; CAD23677.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
FT NON\_TER 1  
FT NON\_TER 123  
FT NON\_TER 123  
SQ SEQUENCE 123 AA; 14895 MW; 489C41C5C275D88F CRC64;  
Query Match 100.0%; Score 139; DB 15; Length 123;  
Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db 17 RILAVERYLKDQQLGIWGCSGKLC 42

RESULT 9  
Q7ZCD7 ID Q7ZCD7 PRELIMINARY; PRT; 144 AA.  
AC Q7ZCD7;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX53-1;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185383; AA05658.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16887 MW; A139DIC53D318EBE CRC64;

Query Match 100.0%; Score 139; DB 15; Length 144;  
Best Local Similarity 100.0%; Pred. No. 1.6e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db 50 RILAVERYLKDQQLGIWGCSGKLC 75

RESULT 10  
Q7ZCD6 ID Q7ZCD6 PRELIMINARY; PRT; 144 AA.  
AC Q7ZCD6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX53-2;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185384; AA05659.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1

FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16907 MW; A427C02C24218EEB CRC64;

Query Match 100.0%; Score 139; DB 15; Length 144;  
Best Local Similarity 100.0%; Pred. No. 1.6e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db 50 RILAVERYLKDQQLGIWGCSGKLC 75

RESULT 11  
Q7ZC52 ID Q7ZC52 PRELIMINARY; PRT; 145 AA.  
AC Q7ZC52;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX18;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B  
RT subtype HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185468; AA065743.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 145 145  
SQ SEQUENCE 145 AA; 17020 MW; AC8C32E97B09D1A1 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 145;  
Best Local Similarity 100.0%; Pred. No. 1.6e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db 48 RILAVERYLKDQQLGIWGCSGKLC 73

RESULT 12  
Q7ZC48 ID Q7ZC48 PRELIMINARY; PRT; 145 AA.  
AC Q7ZC48;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX22;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B  
RT subtype HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY185472; AAO65747.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 145 145  
SQ SEQUENCE 145 AA; 17003 MW; 9CC7F8CD12FBD430 CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 145;  
Best Local Similarity 100.0%; Pred. No. 1.6e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 48 RILAVERYLKDQQLGIWGCSGKLIC 73  
  
RESULT 13  
Q8J3N1  
ID Q8J3N1 PRELIMINARY; PRT; 155 AA.  
AC Q8J3N1;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 protein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22092513; PubMed=12097573;  
RA Boutonnet N., Janssens W., Boutton C., Verschelde J.L., Heyndrickx L.,  
RA Beirnaert E., van der Groen G., Lasters I.;  
RT "Comparison of predicted scaffold-compatible sequence variation in the  
RT triple-hairpin structure of human immunodeficiency virus type 1 gp41  
RT with patient data";  
RL J. Virol. 76:7595-7606(2002).  
DR EMBL; AJ428022; CAD20974.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 155 155  
SQ SEQUENCE 155 AA; 18393 MW; DE623EDD8411EC3 CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 155;  
Best Local Similarity 100.0%; Pred. No. 1.7e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 35 RILAVERYLKDQQLGIWGCSGKLIC 60  
  
RESULT 14  
Q78119  
ID Q78119 PRELIMINARY; PRT; 357 AA.  
AC Q78119;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope protein, gp120 /gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=92144209; PubMed=1736940;  
RA Steuler H., Storch-Hagenlocher B., Wildemann B.;  
RT "Distinct populations of Human immunodeficiency virus type 1 in blood  
RT and cerebrospinal fluid.";  
RL AIDS Res. Hum. Retroviruses 8:53-59(1992).  
DR EMBL; X61356; CAA43624.1; -.  
DR PIR; A53591; A53591.  
DR PIR; S70422; S21996.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 357 AA; 41118 MW; FE4CAA7E122AB8E6 CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 357;  
Best Local Similarity 100.0%; Pred. No. 4.1e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 80 RILAVERYLKDQQLGIWGCSGKLIC 105  
  
RESULT 15  
Q78120  
ID Q78120 PRELIMINARY; PRT; 358 AA.  
AC Q78120;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope protein, gp120/gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92144209; PubMed=1736940;  
RA Steuler H., Storch-Hagenlocher B., Wildemann B.;  
RT "Distinct populations of Human immunodeficiency virus type 1 in blood  
RT and cerebrospinal fluid.";  
RL AIDS Res. Hum. Retroviruses 8:53-59(1992).  
DR EMBL; X61359; CAA43630.1; -.  
DR PIR; S21998; S21998.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 358 AA; 41402 MW; ESE438667785A10D CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 358;  
Best Local Similarity 100.0%; Pred. No. 4.2e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 81 RILAVERYLKDQQLGIWGCSGKLIC 106  
  
RESULT 16  
Q993A8  
ID Q993A8 PRELIMINARY; PRT; 588 AA.  
AC Q993A8;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).



GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA DCosta S.S., Hurwitz J.L.;  
RT "Escape mutants to determine structure of gp120 of HIV-1.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF321147; AAK20295.1; --  
DR PIR; A53591; A53591.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1 588  
FT NON\_TER 588  
SQ SEQUENCE 588 AA; 65643 MW; 47475A5780240AE8 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 588;  
Best Local Similarity 100.0%; Pred. No. 7e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|||||  
Db 522 RILAVERYLKDQQLGIWGCSGKLC 547

RESULT 17  
Q993A7  
ID Q993A7 PRELIMINARY; PRT; 588 AA.  
AC Q993A7;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA DCosta S.S., Hurwitz J.L.;  
RT "Escape mutants to determine structure of gp120 of HIV-1.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF321148; AAK20296.1; --  
DR PIR; A53591; A53591.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1 588  
FT NON\_TER 588  
SQ SEQUENCE 588 AA; 65593 MW; 3FE7610B592EFC6D CRC64;

Query Match 100.0%; Score 139; DB 15; Length 588;  
Best Local Similarity 100.0%; Pred. No. 7e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|||||  
Db 522 RILAVERYLKDQQLGIWGCSGKLC 547

RESULT 18  
Q993B1  
ID Q993B1 PRELIMINARY; PRT; 589 AA.  
AC Q993B1;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1F8;  
RA DCosta S.S., Hurwitz J.L.;  
RT "Escape mutants to determine structure of gp120 of HIV-1.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF321144; AAK20292.1; --  
DR PIR; A53591; A53591.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1 589  
FT NON\_TER 589  
SQ SEQUENCE 589 AA; 65753 MW; 000621646924FD66 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 589;  
Best Local Similarity 100.0%; Pred. No. 7e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|||||  
Db 522 RILAVERYLKDQQLGIWGCSGKLC 547

RESULT 19  
Q993A9  
ID Q993A9 PRELIMINARY; PRT; 590 AA.  
AC Q993A9;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=wt2;  
RA DCosta S.S., Hurwitz J.L.;  
RT "Escape mutants to determine structure of gp120 of HIV-1.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF321146; AAK20294.1; --  
DR PIR; A53591; A53591.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

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FT  NON_TER      1      1
FT  NON_TER      590    590
SQ  SEQUENCE     590 AA;  65902 MW;  91ED899CB8F91CAF CRC64;

  Query Match          100.0%;  Score 139;  DB 15;  Length 590;
  Best Local Similarity 100.0%;  Pred. No. 7e-13;
  Matches 26;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  1 RILAVERYLKDQQLGIWGCSGKLIC 26
    |||||
Db  523 RILAVERYLKDQQLGIWGCSGKLIC 548

RESULT 20
Q993B0
ID  Q993B0      PRELIMINARY;      PRT;      616 AA.
AC  Q993B0;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Envelope glycoprotein (Fragment).
GN  ENV.
OS  Human immunodeficiency virus 1.
OC  Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX  NCBI_TaxID=11676;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1H6;
RA  DCosta S.S., Hurwitz J.L.;
RT  "Escape mutants to determine structure of gp120 of HIV-1.";
RL  Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF321145; AAK20293.1; -.
DR  PIR; A53591; A53591.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0019028; C:viral capsid; IEA.
DR  GO; GO:0019031; C:viral envelope; IEA.
DR  GO; GO:0005198; F:structural molecule activity; IEA.
DR  InterPro; IPR000328; Env GP41.
DR  InterPro; IPR000777; GP120.
DR  Pfam; PF00516; GP120; 1.
DR  Pfam; PF00517; GP41; 1.
KW  AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT  NON_TER      1      1
FT  NON_TER      616    616
SQ  SEQUENCE     616 AA;  69189 MW;  57A8E20F9A580A4F CRC64;

  Query Match          100.0%;  Score 139;  DB 15;  Length 616;
  Best Local Similarity 100.0%;  Pred. No. 7.3e-13;
  Matches 26;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  1 RILAVERYLKDQQLGIWGCSGKLIC 26
    |||||
Db  523 RILAVERYLKDQQLGIWGCSGKLIC 548

RESULT 21
Q993B2
ID  Q993B2      PRELIMINARY;      PRT;      618 AA.
AC  Q993B2;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Envelope glycoprotein (Fragment).
GN  ENV.
OS  Human immunodeficiency virus 1.
OC  Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX  NCBI_TaxID=11676;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1B6;
RA  DCosta S.S., Hurwitz J.L.;
RT  "Escape mutants to determine structure of gp120 of HIV-1.";
RL  Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
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DR  EMBL; AF321143; AAK20291.1; -.
DR  PIR; A53591; A53591.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0019028; C:viral capsid; IEA.
DR  GO; GO:0019031; C:viral envelope; IEA.
DR  GO; GO:0005198; F:structural molecule activity; IEA.
DR  InterPro; IPR000328; Env GP41.
DR  InterPro; IPR000777; GP120.
DR  Pfam; PF00516; GP120; 1.
DR  Pfam; PF00517; GP41; 1.
KW  AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT  NON_TER      1      1
FT  NON_TER      618    618
SQ  SEQUENCE     618 AA;  69364 MW;  B9C791E7D357D2AE CRC64;

  Query Match          100.0%;  Score 139;  DB 15;  Length 618;
  Best Local Similarity 100.0%;  Pred. No. 7.3e-13;
  Matches 26;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  1 RILAVERYLKDQQLGIWGCSGKLIC 26
    |||||
Db  525 RILAVERYLKDQQLGIWGCSGKLIC 550

RESULT 22
Q9Q723
ID  Q9Q723      PRELIMINARY;      PRT;      727 AA.
AC  Q9Q723;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Envelope polyprotein variant.
GN  ENV.
OS  Human immunodeficiency virus 1.
OC  Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX  NCBI_TaxID=11676;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=11Bx;
RX  MEDLINE=9272698; PubMed=10339592;
RA  Hoffman T.L., LaBranch C.C., Zhang W., Canziani G., Robinson J.,
RA  Chaiken I., Hoxie J.A., Doms R.W.;
RT  "Stable exposure of the coreceptor-binding site in a CD4-independent
RT  HIV-1 envelope protein.";
RL  Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=11Bx;
RX  MEDLINE=20027260; PubMed=10559349;
RA  LaBranch C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
RA  Matthews T.J., Doms R.W., Hoxie J.A.;
RT  "Determinants of CD4 independence for a human immunodeficiency virus
RT  type 1 variant map outside regions required for coreceptor
RT  specificity.";
RL  J. Virol. 73:10310-10319(1999).
DR  EMBL; AF189158; AAF25627.1; -.
DR  PIR; A53591; A53591.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0019028; C:viral capsid; IEA.
DR  GO; GO:0019031; C:viral envelope; IEA.
DR  GO; GO:0005198; F:structural molecule activity; IEA.
DR  InterPro; IPR000328; Env GP41.
DR  InterPro; IPR000777; GP120.
DR  Pfam; PF00516; GP120; 1.
DR  Pfam; PF00517; GP41; 1.
KW  AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ  SEQUENCE     727 AA;  82201 MW;  F90FD626D26B9E66 CRC64;

  Query Match          100.0%;  Score 139;  DB 15;  Length 727;
  Best Local Similarity 100.0%;  Pred. No. 8.7e-13;
  Matches 26;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  1 RILAVERYLKDQQLGIWGCSGKLIC 26
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Db          574 RILAVERYLKDQQLLGWCSGKLC 599
|||||
RESULT 23
Q70607      PRELIMINARY;      PRT;      747 AA.
AC Q70607;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-1;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-1;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12034; AAA76669.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732E836A52245F14 CRC64;

Query Match      100.0%; Score 139; DB 15; Length 747;
Best Local Similarity 100.0%; Pred. No. 8.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 RILAVERYLKDQQLLGWCSGKLC 26
|||||
Db          574 RILAVERYLKDQQLLGWCSGKLC 599
|||||
RESULT 24
Q70606      PRELIMINARY;      PRT;      748 AA.
AC Q70606;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW881;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
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RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW881;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12032; AAA76668.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 748
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match      100.0%; Score 139; DB 15; Length 748;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 RILAVERYLKDQQLLGWCSGKLC 26
|||||
Db          575 RILAVERYLKDQQLLGWCSGKLC 600
|||||
RESULT 25
Q70604      PRELIMINARY;      PRT;      752 AA.
AC Q70604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW851;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12030; AAA76666.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match      100.0%; Score 139; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
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Db 579 RILAVERYLKDQQLGIWGCSGKLIC 604

RESULT 26  
Q70605 PRELIMINARY; PRT; 752 AA.  
AC Q70605;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LW852;  
RX MEDLINE=95127297; PubMed=7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker  
RT infected with HIV type 1 (HTLV type IIIB).";  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LW852;  
RX Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBDJ databases.  
DR EMBL; U12031; AAA76667.1; -.  
DR PIR; A53591; A53591.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP41; 1.  
DR Pfam; PF00517; GP120; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 752 752  
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 139; DB 15; Length 752;  
Best Local Similarity 100.0%; Pred. No. 9e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 579 RILAVERYLKDQQLGIWGCSGKLIC 604

RESULT 27  
Q70608 PRELIMINARY; PRT; 752 AA.  
AC Q70608;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LW87-2;  
RX MEDLINE=95127297; PubMed=7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker

RT infected with HIV type 1 (HTLV type IIIB).";  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LW87-2;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBDJ databases.  
DR EMBL; U12035; AAA76670.1; -.  
DR PIR; A53591; A53591.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 752 752  
SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0B8F8 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 752;  
Best Local Similarity 100.0%; Pred. No. 9e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 579 RILAVERYLKDQQLGIWGCSGKLIC 604

RESULT 28  
Q9Q722 PRELIMINARY; PRT; 757 AA.  
AC Q9Q722;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope polyprotein variant.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IIIBx;  
RX MEDLINE=99272698; PubMed=10339592;  
RA Hoffman T.L., LaBranche C.C., Zhang W., Canziani G., Robinson J.,  
RA Chaiken I., Hoxie J.A., Doms R.W.;  
RT "Stable exposure of the coreceptor-binding site in a CD4-independent  
RT HIV-1 envelope protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IIIBx;  
RX MEDLINE=20027260; PubMed=10559349;  
RA LaBranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,  
RA Matthews T.J., Doms R.W., Hoxie J.A.;  
RT "Determinants of CD4 independence for a human immunodeficiency virus  
RT type 1 variant map outside regions required for coreceptor  
RT specificity.";  
RL J. Virol. 73:10310-10319(1999).  
DR EMBL; AF189159; AAF25628.1; -.  
DR PIR; A53591; A53591.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR InterPro; IPR000625; REV\_protein.



DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
DR Pfam; PF00424; REV; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 757 AA; 85539 MW; A758AF8D8263BD2E CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 757;  
Best Local Similarity 100.0%; Pred. No. 9.1e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 574 RILAVERYLKDQQLGIWGCSGKLIC 599  
  
RESULT 29  
Q9WMV1 PRELIMINARY; PRT; 800 AA.  
AC Q9WMV1;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope (Gp160) (Fragment).  
GN ENV OR GP160.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MP255;  
RX MEDLINE=99294894; PubMed=10364493;  
RA Triques K., Bourgeois A., Saragosti S., Vidal N., Mpoudi-Ngole E.,  
RA Nzilambi N., Apetrei C., Ekwilanga M., Delaporte E., Peeters M.;  
RT "High diversity of HIV-1 subtype F strains in Central Africa.";  
RL Virology 259:99-109(1999).  
DR EMBL; AJ237805; CAB44056.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 800  
SQ SEQUENCE 800 AA; 90612 MW; 79A7EA536AFAFEC1 CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 800;  
Best Local Similarity 100.0%; Pred. No. 9.6e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 533 RILAVERYLKDQQLGIWGCSGKLIC 558  
  
RESULT 30  
Q9WMU9 PRELIMINARY; PRT; 801 AA.  
AC Q9WMU9;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope (Gp160) (Fragment).  
GN ENV OR GP160.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MP535;  
  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
DR Pfam; PF00424; REV; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 800  
SQ SEQUENCE 800 AA; 90612 MW; 79A7EA536AFAFEC1 CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 800;  
Best Local Similarity 100.0%; Pred. No. 9.6e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 533 RILAVERYLKDQQLGIWGCSGKLIC 558  
  
RESULT 30  
Q9WMU9 PRELIMINARY; PRT; 801 AA.  
AC Q9WMU9;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope (Gp160) (Fragment).  
GN ENV OR GP160.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MP535;

RX MEDLINE=99294894; PubMed=10364493;  
RA Triques K., Bourgeois A., Saragosti S., Vidal N., Mpoudi-Ngole E.,  
RA Nzilambi N., Apetrei C., Ekwilanga M., Delaporte E., Peeters M.;  
RT "High diversity of HIV-1 subtype F strains in Central Africa.";  
RL Virology 259:99-109(1999).  
DR EMBL; AJ237807; CAB44058.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 801  
SQ SEQUENCE 801 AA; 90521 MW; 9AEE71C1C840A88B CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 801;  
Best Local Similarity 100.0%; Pred. No. 9.6e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 534 RILAVERYLKDQQLGIWGCSGKLIC 559  
  
RESULT 31  
Q8QX2 PRELIMINARY; PRT; 807 AA.  
AC Q8QX2;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Gorry P.R., Taylor J., Holm G., Mehle A., Morgan T., Cayabyab M.,  
RA Farzan M., Wang H., Bell J.E., Kunstman K.J., Moore J.P.,  
RA Wolinsky S.M., Gabuzda D.;  
RT "Increased CCR5 affinity and reduced CCR5/CD4 dependence of a  
RT neurovirulent primary human immunodeficiency virus type 1 isolate.";  
RL J. Virol. 0:0-0(2002).  
DR EMBL; AF491740; AAM09793.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 807 AA; 91808 MW; 4B52479155EF5603 CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 807;  
Best Local Similarity 100.0%; Pred. No. 9.7e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 590 RILAVERYLKDQQLGIWGCSGKLIC 615  
  
RESULT 32  
Q9WMV0 PRELIMINARY; PRT; 809 AA.  
ID Q9WMV0  
AC Q9WMV0;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope (Gp160) (Fragment).  
GN ENV OR GP160.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MP257;  
RX MEDLINE=99294894; PubMed=10364493;  
RA Triques K., Bourgeois A., Saragosti S., Vidal N., Mpoudi-Ngole E.,  
RA Nzilambi N., Apetrei C., Ekwilanga M., Delaporte E., Peeters M.;  
RT "High diversity of HIV-1 subtype F strains in Central Africa.";  
RL Virology 259:99-109(1999).  
DR EMBL; AJ237806; CAB44057.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 809 809  
SQ SEQUENCE 809 AA; 91516 MW; 24F5179F72B08F1A CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 809;  
Best Local Similarity 100.0%; Pred. No. 9.7e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCSGKLC 26  
Db 542 RILAVERYLKDQQLGIWCSGKLC 567  
  
RESULT 33  
Q9DVL1 PRELIMINARY; PRT; 826 AA.  
ID Q9DVL1  
AC Q9DVL1  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope protein (Fragment).  
GN ENV OR GP160.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=97DC.KTB22;  
RX MEDLINE=20499072; PubMed=11044094;  
RA Vidal N., Peeters M., Mulanga-Kabeya C., Nzilambi N., Robertson D.,  
RA Ilunga W., Sena H., Tshimanga K., Bongo B., Delaporte E.;  
RT "Unprecedented degree of human immunodeficiency virus Type 1 (HIV-1)  
RT group M genetic diversity in the Democratic Republic of Congo suggests  
RT that the HIV-1 pandemic originated in Central Africa.";  
RL J. Virol. 74:10498-10507(2000).  
DR EMBL; AJ401042; CAC15050.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 826 826

SQ SEQUENCE 826 AA; 93694 MW; 344AF31B694B6883 CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 826;  
Best Local Similarity 100.0%; Pred. No. 9.9e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCSGKLC 26  
Db 566 RILAVERYLKDQQLGIWCSGKLC 591  
  
RESULT 34  
Q9ID89 PRELIMINARY; PRT; 845 AA.  
ID Q9ID89  
AC Q9ID89  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE ENV protein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=95127;  
RA Montavon C., Delaporte E., Peeters M.;  
RT "Two new complete genomes of HIV-1 recombinant AGJ BFP90-like  
RT circulating in Mali and Senegal.";  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ288982; CAB98175.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 845 AA; 95239 MW; 39439B37713EBD2A CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 845;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCSGKLC 26  
Db 568 RILAVERYLKDQQLGIWCSGKLC 593  
  
RESULT 35  
Q69996 PRELIMINARY; PRT; 847 AA.  
ID Q69996  
AC Q69996  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=594;  
RX MEDLINE=96190564; PubMed=8627686;  
RA Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S.,  
RA Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,  
RA von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,  
RA Hahn B.H.;  
RT "Molecular cloning and analysis of functional envelope genes from  
RT human immunodeficiency virus type 1 sequence subtypes A through G. The

RT WHO and NIAID Networks for HIV Isolation and Characterization.";

RL J. Virol. 70:1651-1657(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=594;

RA NIAID/NIH DAIDS Variation Program;

RL Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=594;

RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.

DR EMBL; U08445; AAB04071.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

FT NON TER 1

SQ SEQUENCE 847 AA; 95602 MW; FCBCEA7AF446FB20 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 847;

Best Local Similarity 100.0%; Pred. No. 1e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLLIC 26

Db 570 RILAVERYLKDQQLGIWCSGKLLIC 595

RESULT 36

Q9YKT7

ID Q9YKT7 PRELIMINARY; PRT; 849 AA.

AC Q9YKT7;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Env.

GN Env.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C-96BW05.02;

RX MEDLINE=99214383; PubMed=10196340;

RA Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,

RA Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,

RA Essex M.;

RT "Molecular cloning and phylogenetic analysis of human immunodeficiency

RT virus type 1 subtype C: a set of 23 full-length clones from

RT Botswana.";

RL J. Virol. 73:4427-4432(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C-96BW05.02;

RA Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,

RA Foley B.T., Ndung'u T.P., Marlink R., Essex M.;

RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF110967; AAD17078.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

SQ SEQUENCE 849 AA; 96239 MW; 40BE606217AE2915 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 849;

Best Local Similarity 100.0%; Pred. No. 1e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLLIC 26

Db 572 RILAVERYLKDQQLGIWCSGKLLIC 597

RESULT 37

Q90CI9

ID Q90CI9 PRELIMINARY; PRT; 849 AA.

AC Q90CI9;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Envelope glycoprotein.

GN Env.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CM53657;

RX MEDLINE=21342588; PubMed=11448170;

RA Carr J.K., Torimiro J.N., Wolfe N.D., Eitel M.N., Kim B.,

RA Sanders-Buell E., Jagodzinski L.L., Gotte D., Burke D.S., Birx D.L.,

RA McCutchan F.E.;

RT "The AG recombinant IBNG and novel strains of group M HIV-1 are common

RT in Cameroon.";

RL Virology 286:168-181(2001).

DR EMBL; AF377956; AAK59195.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

SQ SEQUENCE 849 AA; 95476 MW; 898B30FA6ECCE3DC CRC64;

Query Match 100.0%; Score 139; DB 15; Length 849;

Best Local Similarity 100.0%; Pred. No. 1e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLLIC 26

Db 572 RILAVERYLKDQQLGIWCSGKLLIC 597

RESULT 38

Q9YKT4

ID Q9YKT4 PRELIMINARY; PRT; 849 AA.

AC Q9YKT4;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Env.

GN Env.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C-96BW05.04;

RX MEDLINE=99214383; PubMed=10196340;

RA Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,

RA Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,

RA Essex M.;







RX MEDLINE=96036482; PubMed=7483282;  
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,  
RA Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;  
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes  
RT from primary virus cultures using the polymerase chain reaction.";  
RL Virology 213:80-86(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NL4-3;  
RX MEDLINE=86281827; PubMed=3016298;  
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
RA Martin M.A.;  
RT "Production of acquired immunodeficiency syndrome-associated  
RT retrovirus in human and nonhuman cells transfected with an infectious  
RT molecular clone.";  
RL J. Virol. 59:284-291(1986).  
DR EMBL; U26942; AAB60578.1; -.  
DR PIR; A53591; A53591.  
DR PIR; S13288; S13288.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT CONFLICT 214 214 H -> L (IN REF. 2).  
FT CONFLICT 530 530 A -> S (IN REF. 2).  
FT CONFLICT 739 739 G -> D (IN REF. 2).  
SQ SEQUENCE 854 AA; 97005 MW; FF2264H3841D1220 CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 854;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 577 RILAVERYLKDQQLGIWGCSGKLIC 602  
  
RESULT 45  
Q90178  
ID O90178 PRELIMINARY; PRT; 854 AA.  
AC O90178;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95074930; PubMed=7983770;  
RA Fang H., Pincus S.H.;  
RT "Unique insertion sequence and pattern of CD4 expression in variants  
RT selected with immunotoxins from human immunodeficiency virus type 1-  
RT infected T cells.";  
RL J. Virol. 69:75-81(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Fang H., Pincus S.H.;  
RT "Spontaneous activation of human immunodeficiency virus type 1 in an  
RT immunotoxin-resistant variant T cell line.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070521; AAC28452.1; -.  
DR PIR; A53591; A53591.  
DR PIR; S13288; S13288.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 854;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 577 RILAVERYLKDQQLGIWGCSGKLIC 602  
  
RESULT 46  
Q9DVL2  
ID Q9DVL2 PRELIMINARY; PRT; 854 AA.  
AC Q9DVL2;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope protein (Fragment).  
GN ENV OR GP160.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=J\_97DC.KTB147;  
RX MEDLINE=20499072; PubMed=11044094;  
RA Vidal N., Peeters M., Mulanga-Kabeya C., Nzilambi N., Robertson D.,  
RA Ilunga W., Sema H., Tshimanga K., Bongo B., Delaporte E.;  
RT "Unprecedented degree of human immunodeficiency virus Type 1 (HIV-1)  
RT group M genetic diversity in the Democratic Republic of Congo suggests  
RT that the HIV-1 pandemic originated in Central Africa.";  
RL J. Virol. 74:10498-10507(2000).  
DR EMBL; AJ401041; CAC15049.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1  
SQ SEQUENCE 854 AA; 96040 MW; 5A13A29231B0EDCF CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 854;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 577 RILAVERYLKDQQLGIWGCSGKLIC 602  
  
RESULT 47  
Q78705  
ID Q78705 PRELIMINARY; PRT; 854 AA.  
AC Q78705;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein gp120.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

```
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96013815; PubMed=7474132;
RA Duensing T.D., Fang H., Dorward D.W., Pincus S.H.;
RT "Processing of the envelope glycoprotein gp160 in immunotoxin-
RT resistant cell lines chronically infected with human immunodeficiency
RT virus type 1.";
RL J. Virol. 69:7122-7131(1995).
DR EMBL; L42371; AAA96326.1; -.
DR PIR; A53591; A53591.
DR PIR; S13288; S13288.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 854 AA; 97199 MW; 5B9512216533E256 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 854;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db |||||
577 RILAVERYLKDQQLGIWGCSGKLIC 602

RESULT 48
Q8AQV7 ID Q8AQV7 PRELIMINARY; PRT; 855 AA.
AC Q8AQV7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Lemey P., Salemi M., Wang B., Saksena N.K., Vandamme A.M.;
RT "Maximum Likelihood Analysis of Clock-Like Behavior in HIV:
RT Implications on Dating Strategies in HIV Molecular Phylogenies.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF538302; AAN64079.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
SQ SEQUENCE 855 AA; 97180 MW; 81887BBFAD516F27 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 855;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db |||||
578 RILAVERYLKDQQLGIWGCSGKLIC 603

RESULT 49
Q74090 ID Q74090 PRELIMINARY; PRT; 856 AA.
AC Q74090;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Env.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM213;
RX MEDLINE=90101366; PubMed=1688473;
RA Cloyd M.W., Moore B.E.;
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
RT (HIV-1) Isolates.";
RL Virology 174:103-116(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PM213;
RA Iwatani Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D86069; BAA13003.1; -.
DR PIR; A53591; A53591.
DR PIR; S13288; S13288.
DR PDB; 1F23; 20-JUN-01.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 100.0%; Score 139; DB 15; Length 856;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db |||||
579 RILAVERYLKDQQLGIWGCSGKLIC 604

RESULT 50
O92877 ID O92877 PRELIMINARY; PRT; 856 AA.
AC O92877;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99098984; PubMed=9882298;
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,
RA Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,
RA Sodroski J.G.;
RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins
RT responsible for the pathogenicity of a multiply passaged simian-human
RT immunodeficiency virus (SHIV-HXBc2).";
RL J. Virol. 73:976-984(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,
RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041850; AAD12142.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
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DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 856 AA; 97151 MW; C50BE0388FB73659 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 856;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 579 RILAVERYLKDQQLGIWGCSGKLIC 604

RESULT 51  
Q74599 PRELIMINARY; PRT; 856 AA.  
AC Q74599;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Env.  
GN Env.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MCK1;  
RX MEDLINE=90101366; PubMed=1688473;  
RA Cloyd M.W., Moore B.E.;  
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus (HIV-1) Isolates.";  
RL Virology 174:103-116(1990).  
RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=MCK1;  
RA Iwatani Y.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; D86068; BAA12995.1; -.  
DR PIR; A53591; A53591.  
DR PIR; S13288; S13288.  
DR PDB; 1F23; 20-JUN-01.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 856;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 579 RILAVERYLKDQQLGIWGCSGKLIC 604

RESULT 52  
O92822 PRELIMINARY; PRT; 857 AA.  
ID O92822  
AC O92822;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein.  
GN Env.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ACH168.10;  
RX MEDLINE=95074890; PubMed=7983734;  
RA Wrin T., Loh T.P., Vennari J.C., Schuitemaker H., Nunberg J.H.;  
RT "Adaptation to persistent growth in the H9 cell line renders a primary isolate of human immunodeficiency virus type 1 sensitive to neutralization by vaccine sera.";  
RL J. Virol. 69:39-48(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ACH168.10;  
RA LaCasse R.A., Follis K.E., Moudgil T., Trahey M., Binley J.M., Planelles V., Zolla-Pazner S., Nunberg J.H.;  
RT "Coreceptor utilization by human immunodeficiency virus type 1 is not a primary determinant of neutralization sensitivity.";  
RL J. Virol. 0:0-0(1997).  
DR EMBL; AF035533; AAB99954.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 857 AA; 97370 MW; 3EB213BD2DCD485D CRC64;

Query Match 100.0%; Score 139; DB 15; Length 857;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 580 RILAVERYLKDQQLGIWGCSGKLIC 605

RESULT 53  
Q71013 PRELIMINARY; PRT; 857 AA.  
ID Q71013  
AC Q71013;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein.  
GN Env.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168C;  
RX MEDLINE=95074890; PubMed=7983734;  
RA Wrin T., Loh T.P., Vennari J.C., Schuitemaker H., Nunberg J.H.;  
RT "Adaptation to persistent growth in the H9 cell line renders a primary isolate of human immunodeficiency virus type 1 sensitive to neutralization by vaccine sera.";  
RL J. Virol. 69:39-48(1995).  
DR EMBL; U15031; AAA64869.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.





Best Local Similarity 100.0%; Pred. No. 1e-12; Mismatches 0; Indels 0; Gaps 0; Matches 26; Conservative 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLLC 26  
|||||  
Db 580 RILAVERYLKDQQLGIWGCSGKLLC 605

RESULT 57

Q9YUZ4  
ID Q9YUZ4 PRELIMINARY; PRT; 859 AA.  
AC Q9YUZ4;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SE6594;  
RX MEDLINE=99441797; PubMed=10513639;  
RA Carr J.K., Laukkanen T., Salminen M.O., Albert J., Alaeus A., Kim B.,  
RA Sanders-Buell E., Birx D.L., McCutchan F.E.;  
RT "Characterization of subtype A HIV-1 from Africa by full genome  
RT sequencing.";  
RL AIDS 13:1819-1826(1999).  
DR EMBL; AF069672; AAD13364.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 859 AA; 96945 MW; B49458013BA96EB9 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 859;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLLC 26  
|||||  
Db 575 RILAVERYLKDQQLGIWGCSGKLLC 600

RESULT 58

Q9WLJ1  
ID Q9WLJ1 PRELIMINARY; PRT; 859 AA.  
AC Q9WLJ1;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BFP90;  
RX MEDLINE=99039935; PubMed=9824329;  
RA Oelrichs R.B., Workman C., Laukkanen T., McCutchan F.E., Deacon N.J.;  
RT "A novel subtype A/G/J recombinant full-length HIV type 1 genome from  
RT Burkina Faso.";  
RL AIDS Res. Hum. Retroviruses 14:1495-1500(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BFP90;

Query Match 100.0%; Score 139; DB 15; Length 859;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RA Oelrichs R.B.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBDJ databases.  
DR EMBL; AF064699; AAD03314.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 859 AA; 96504 MW; 41BB25F110C38E0C CRC64;

Query Match 100.0%; Score 139; DB 15; Length 859;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLLC 26  
|||||  
Db 582 RILAVERYLKDQQLGIWGCSGKLLC 607

RESULT 59

Q7SQA7  
ID Q7SQA7 PRELIMINARY; PRT; 860 AA.  
AC Q7SQA7;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=subtype A;  
RA Tatsumi M., Matsuda M.;  
RT "Infectious DNA clones of HIV-1 subtype A.";  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBDJ databases.  
DR EMBL; AB098332; BAC77753.1; --  
KW Envelope protein.  
SQ SEQUENCE 860 AA; 97452 MW; E694AF763073A6DD CRC64;

Query Match 100.0%; Score 139; DB 15; Length 860;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLLC 26  
|||||  
Db 575 RILAVERYLKDQQLGIWGCSGKLLC 600

RESULT 60

Q8UNL9  
ID Q8UNL9 PRELIMINARY; PRT; 862 AA.  
AC Q8UNL9;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=X605;

RA Delgado E., Thomson M.M., Villahermosa M.L., Sierra M., Ocampo A.,  
RA Miralles C., Rodriguez-Perez R., Diz-Aren J., Ojea-de-Castro R.,  
RA Losada E., Cuevas M.T., Vazquez de Parga E., Carmona R.,  
RA Perez Alvarez L., Medrano L., Cuevas L., Taboada J.A., Najera R.;

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RT "Identification of a newly characterized HIV-1 BG intersubtype
RT Circulating Recombinant Form in Galicia, Spain, exhibiting a
RT pseudotype-like virion structure.";
RL J. Acquir. Immune Defic. Syndr. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=X605;
RA Delgado E., Thomson M.M., Villahermosa M.L., Sierra M., Ocampo A.,
RA Miralles C., Rodriguez-Perez R., Diz-Aren J., Ojea-de-Castro R.,
RA Losada E., Cuevas M.T., Vazquez de Parga E., Carmona R.,
RA Perez Alvarez L., Medrano L., Cuevas L., Taboada J.A., Najera R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF450096; AAL47033.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 862 AA; 98014 MW; E7AF58E5E939F2B CRC64;

Query Match 100.0%; Score 139; DB 15; Length 862;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db |||||
578 RILAVERYLKDQQLGIWGCSGKLC 603

RESULT 61
Q7SQA2 PRELIMINARY; PRT; 862 AA.
AC Q7SQA2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=subtype A;
RA Tatsumi M., Matsuda M.;
RT "Infectious DNA clones of HIV-1 subtype A.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB098333; BAC77762.1; -.
KW Envelope protein.
SQ SEQUENCE 862 AA; 97469 MW; CB46A4D2982F606E CRC64;

Query Match 100.0%; Score 139; DB 15; Length 862;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db |||||
577 RILAVERYLKDQQLGIWGCSGKLC 602

RESULT 62
Q9YP39 PRELIMINARY; PRT; 864 AA.
AC Q9YP39;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polyprotein.
GN ENV.
```

```
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Fang G., Weiser B., Chappey C., Visosky A., Townsend L., Wang Q.,
RA Burger H.;
RT "Complete Plasma HIV-1 Sequence: Spl-Promoter Deletion Can Lead to
RT Non-Progressive Infection.";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U69589; AAD10915.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 864 AA; 98272 MW; C29EE033EE9D2D99 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 864;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db |||||
587 RILAVERYLKDQQLGIWGCSGKLC 612

RESULT 63
Q7ZJC8 PRELIMINARY; PRT; 864 AA.
AC Q7ZJC8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US4;
RA Carr J.K., Hierholzer J., Montano S., Hoelscher M., Negrete M.,
RA Hierholzer M., Avila M., Gomez Carrillo M., Russi J., Vinales J.,
RA Alava A., Acosta M., Gianella A., Andrade R., Sanchez J.L.,
RA Carrion G., Sanchez J., Robb M., Birx D., McCutchan F.;
RT "Molecular Epidemiology of HIV type 1 in Ecuador, Peru, Bolivia,
RT Uruguay and Argentina.";
RL AIDS Res. Hum. Retroviruses 0:0-0(2003).
DR EMBL; AY173955; AA063221.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
SQ SEQUENCE 864 AA; 97752 MW; 87B26D13FC93552E CRC64;

Query Match 100.0%; Score 139; DB 15; Length 864;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db |||||
587 RILAVERYLKDQQLGIWGCSGKLC 612

RESULT 64
```

Q9WPZ4 Q9WPZ4 PRELIMINARY; PRT; 866 AA.  
AC Q9WPZ4;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope protein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99236722; PubMed=10221533;  
RA Quinlan G.V. Jr., Zhang P.F., Fu D.W., Dong M., Alter H.J.;  
RT "Expression and characterization of HIV type 1 envelope protein associated with a broadly reactive neutralizing antibody response.";  
RL AIDS Res. Hum. Retroviruses 15:561-570(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Quinlan G.V. Jr., Zhang P.F., Fu D.W., Dong M., Alter H.J.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF128126; AAD40637.2; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
SQ SEQUENCE 866 AA; 98081 MW; 44D9329789833122 CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 866;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db 588 RILAVERYLKDQQLGIWGCSGKLC 613  
  
RESULT 65  
Q8ADN9 Q8ADN9 PRELIMINARY; PRT; 868 AA.  
AC Q8ADN9;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=99UGK30889;  
RX MEDLINE=22375625; PubMed=12487816;  
RA Harris M.E., Serwadda D., Sewankambo N., Wabwire F., Kim B.,  
RA Kigozi G., Kiwanuka N., Phillips J.B., Meehen M., Lutalo T.,  
RA Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L.,  
RA McCutchan F.E.;  
RT "Among 46 Near Full Length HIV Type 1 Genome Sequences from Rakai District, Uganda, Subtype D and AD Recombinants Predominate.";  
RL AIDS Res. Hum. Retroviruses 18:1281-1290(2002).  
DR EMBL; AF484501; AAN73652.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.

SQ SEQUENCE 868 AA; 98621 MW; 5EFD3B73746F13 CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 868;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db 584 RILAVERYLKDQQLGIWGCSGKLC 609  
  
RESULT 66  
Q8Q2X1 Q8Q2X1 PRELIMINARY; PRT; 870 AA.  
AC Q8Q2X1;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Gorry P.R., Taylor J., Holm G., Mehle A., Morgan T., Cayabyab M.,  
RA Farzan M., Wang H., Bell J.E., Kunstman K.J., Moore J.P.,  
RA Wolinsky S.M., Gabuzda D.;  
RT "Increased CCR5 affinity and reduced CCR5/CD4 dependence of a neurovirulent primary human immunodeficiency virus type 1 isolate.";  
RL J. Virol. 0:0-0(2002).  
DR EMBL; AF491741; AAM09794.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
SQ SEQUENCE 870 AA; 99067 MW; 067C44F6526160DF CRC64;  
  
Query Match 100.0%; Score 139; DB 15; Length 870;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db 593 RILAVERYLKDQQLGIWGCSGKLC 618  
  
RESULT 67  
Q8Q2X0 Q8Q2X0 PRELIMINARY; PRT; 870 AA.  
AC Q8Q2X0;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Gorry P.R., Taylor J., Holm G., Mehle A., Morgan T., Cayabyab M.,  
RA Farzan M., Wang H., Bell J.E., Kunstman K.J., Moore J.P.,  
RA Wolinsky S.M., Gabuzda D.;  
RT "Increased CCR5 affinity and reduced CCR5/CD4 dependence of a neurovirulent primary human immunodeficiency virus type 1 isolate.";  
RL J. Virol. 0:0-0(2002).  
DR EMBL; AF491742; AAM09795.1; -.



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DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019028; C:viral capsid; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 870 AA; 98932 MW; 924EE3A64FD6A9B1 CRC64;

Query Match      100.0%; Score 139; DB 15; Length 870;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 593 RILAVERYLKDQQLGIWGCSGKLIC 618

RESULT 68
Q8AEX3
ID Q8AEX3 PRELIMINARY; PRT; 94 AA.
AC Q8AEX3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,
RA Germano de Sousa J., Canas-Ferreira W.;
RT "Genetic diversity of HIV-1 spreading among intravenous drug users in
RT Lisbon, Portugal.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AJ429040; CAD23676.1; -.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
SQ SEQUENCE 94 AA; 11165 MW; B59B27115A79E800 CRC64;

Query Match      99.3%; Score 138; DB 15; Length 94;
Best Local Similarity 96.2%; Pred. No. 1.5e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 17 RVLAVERYLKDQQLGIWGCSGKLIC 42

RESULT 69
O40239
ID O40239 PRELIMINARY; PRT; 109 AA.
AC O40239;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Transmembrane glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=12721;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MP109;
RA Burin des Roziers N., Coste J., Courouce A.M., Bibollet-Ruche F.,
RA Guillard O., Nasr O.;
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RT "Detection of HIV-1 RNA in two consecutive blood donations screened
RT negative for HIV-antibody.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBDJ databases.
DR EMBL; Y11839; CAA72537.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 12705 MW; CDE3D9FE5574175E CRC64;

Query Match      99.3%; Score 138; DB 15; Length 109;
Best Local Similarity 96.2%; Pred. No. 1.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 9 RVLAVERYLKDQQLGIWGCSGKLIC 34

RESULT 70
Q8UQW2
ID Q8UQW2 PRELIMINARY; PRT; 112 AA.
AC Q8UQW2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98ZM044F;
RX MEDLINE=21602569; PubMed=11739704;
RA Trask S.A., Derdeyn C.A., Fideli U., Chen Y., Meleth S., Kasolo F.,
RA Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
RT transmission in a heterosexual cohort of discordant couples in
RT Zambia.";
RL J. Virol. 76:397-405 (2002).
DR EMBL; AF405196; AAL66706.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 13435 MW; E27EB83B15703197 CRC64;

Query Match      99.3%; Score 138; DB 15; Length 112;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 15 RILAVERYLKDQQLGIWGCSGKLIC 40

RESULT 71
Q9QQN5
ID Q9QQN5 PRELIMINARY; PRT; 117 AA.
AC Q9QQN5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
```

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GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USHIPS7;
RA Ellenberger D.; Sullivan P.S.; Dorn J.; Schable C.; Spira T.J.;
RA Folks T.M.; Lal R.B.;
RT "Viral and Immunologic Examination of HIV-1-infected Persistently
RT Seronegative (HIPS) Persons.";
RL J. Infect. Dis. 0:0-0(1999).
DR EMBL; AF157468; AAD45888.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 14011 MW; 9A71687C21470E60 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db |:|||||
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 72
Q9YRT2
ID Q9YRT2 PRELIMINARY; PRT; 117 AA.
AC Q9YRT2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USNG15;
RA Sullivan P.J.; Do A.; Ellenberger D.L.; Pau C.-P.; Paul S.; Kalish M.;
RA Robbins K.; Lal R.; Storck C.; Schable C.A.; Wise H.; Tetteh C.;
RA Jones J.; Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096334; AAD04409.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13959 MW; DED23BB002B524D9 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db |:|||||
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 73
Q9YRS4
ID Q9YRS4 PRELIMINARY; PRT; 117 AA.
AC Q9YRS4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USNG46;
RA Sullivan P.J.; Do A.; Ellenberger D.L.; Pau C.-P.; Paul S.; Kalish M.;
RA Robbins K.; Lal R.; Storck C.; Schable C.A.; Wise H.; Tetteh C.;
RA Jones J.; Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096342; AAD04417.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13920 MW; 39BD6AAE4FAD37AA CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db |:|||||
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 74
Q9QQN0
ID Q9QQN0 PRELIMINARY; PRT; 117 AA.
AC Q9QQN0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USHIPS9;
RA Ellenberger D.; Sullivan P.S.; Dorn J.; Schable C.; Spira T.J.;
RA Folks T.M.; Lal R.B.;
RT "Viral and Immunologic Examination of HIV-1-infected Persistently
RT Seronegative (HIPS) Persons.";
RL J. Infect. Dis. 0:0-0(1999).
DR EMBL; AF157473; AAD45893.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13917 MW; E7DBBF9364538256 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
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Best Local Similarity 96.2%; Pred. No. 1.8e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 75  
Q9YZ04 PRELIMINARY; PRT; 117 AA.  
AC Q9YZ04;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=135.544;  
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,  
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;  
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in  
RT Uganda";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF006864; AAD01308.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 117  
SQ SEQUENCE 117 AA; 13970 MW; AACAA0502CE79044A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;  
Best Local Similarity 96.2%; Pred. No. 1.8e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 23 RVLAVERYLKDQQLGIWGCSGKLC 48

RESULT 76  
Q9YRS6 PRELIMINARY; PRT; 117 AA.  
AC Q9YRS6;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=96USSN19;  
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,  
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,  
RA Jones J., Ward J.;  
RT "Surveillance of Central African Nationals living in the United States  
RT reveals multiple subtypes of HIV-1 Group M and Group O.";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF096340; AAD04415.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 117  
SQ SEQUENCE 117 AA; 13864 MW; C8P2F6CBC0A5437F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;  
Best Local Similarity 96.2%; Pred. No. 1.8e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 77  
Q9WKU0 PRELIMINARY; PRT; 117 AA.  
AC Q9WKU0;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=96USNG19;  
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,  
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,  
RA Jones J., Ward J.;  
RT "Surveillance of Central African Nationals living in the United States  
RT reveals multiple subtypes of HIV-1 Group M and Group O.";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF096333; AAD04408.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 117  
SQ SEQUENCE 117 AA; 13959 MW; BBA0CA6FDE179EBC CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;  
Best Local Similarity 96.2%; Pred. No. 1.8e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 78  
Q9WM72 PRELIMINARY; PRT; 117 AA.  
AC Q9WM72;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=140.330;  
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,

RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;  
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in  
RL Uganda."; NCBI\_TaxID=11676;  
DR EMBL; AF006868; AAD01312.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 13954 MW; 423078A5169EB536 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 117;  
Best Local Similarity 96.2%; Pred. No. 1.8e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 23 RVLAVERYLKDQQLGIWGCSGKLIC 48  
  
RESULT 79  
Q9QQN3  
ID Q9QQN3 PRELIMINARY; PRT; 117 AA.  
AC Q9QQN3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=96USHIPS2;  
RA Ellenberger D.; Sullivan P.S., Dorn J., Schable C., Spira T.J.,  
RA Folks T.M., Lal R.B.;  
RT "Viral and Immunologic Examination of HIV-1-infected Persistently  
RT Seronegative (HIPS) Persons.";  
RL J. Infect. Dis. 0:0-0(1999).  
DR EMBL; AF157470; AAD45890.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 14008 MW; 94D6279CB86297B0 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 117;  
Best Local Similarity 96.2%; Pred. No. 1.8e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44  
  
RESULT 80  
Q9YZ01  
ID Q9YZ01 PRELIMINARY; PRT; 117 AA.  
AC Q9YZ01;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=161.287;  
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,  
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;  
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in  
RT Uganda."; NCBI\_TaxID=11676;  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF006872; AAD01316.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 13950 MW; C3C550C19DDB602E6 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 117;  
Best Local Similarity 96.2%; Pred. No. 1.8e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 23 RVLAVERYLKDQQLGIWGCSGKLIC 48  
  
RESULT 81  
Q9YRS2  
ID Q9YRS2 PRELIMINARY; PRT; 117 AA.  
AC Q9YRS2;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=96USTG17;  
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,  
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,  
RA Jones J., Ward J.;  
RT "Surveillance of Central African Nationals living in the United States  
RT reveals multiple subtypes of HIV-1 Group M and Group O.";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF096344; AAD04419.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 14004 MW; 11CA37F5C8C6278F CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 117;  
Best Local Similarity 96.2%; Pred. No. 1.8e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44  
  
RESULT 82



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Q9YYZ2
ID Q9YYZ2 PRELIMINARY; PRT; 117 AA.
AC Q9YYZ2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=204.987;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006894; AAD01338.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13948 MW; 7FA9BE6B7BF8B39E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 23 RVLAVERYLKDQQLGIWGCSGKLIC 48

RESULT 83
Q7SVI8
ID Q7SVI8 PRELIMINARY; PRT; 117 AA.
AC Q7SVI8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG681;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102796; AAM51891.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14076 MW; F9B2B5A3C415C6F6 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 84
Q7SVI4
ID Q7SVI4 PRELIMINARY; PRT; 117 AA.
AC Q7SVI4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG1071;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102800; AAM51895.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14009 MW; B4D300DDB4E0A488 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 85
Q7SVG4
ID Q7SVG4 PRELIMINARY; PRT; 117 AA.
AC Q7SVG4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG619;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102820; AAM51915.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14041 MW; C4195A821EEBB169 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 86
Q7SVG1
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```
Q9YYZ2
ID Q9YYZ2 PRELIMINARY; PRT; 117 AA.
AC Q9YYZ2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=204.987;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006894; AAD01338.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13948 MW; 7FA9BE6B7BF8B39E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 23 RVLAVERYLKDQQLGIWGCSGKLIC 48

RESULT 83
Q7SVI8
ID Q7SVI8 PRELIMINARY; PRT; 117 AA.
AC Q7SVI8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG681;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102796; AAM51891.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14076 MW; F9B2B5A3C415C6F6 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 84
Q7SVI4
ID Q7SVI4 PRELIMINARY; PRT; 117 AA.
AC Q7SVI4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG1071;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102800; AAM51895.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14009 MW; B4D300DDB4E0A488 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 85
Q7SVG4
ID Q7SVG4 PRELIMINARY; PRT; 117 AA.
AC Q7SVG4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG619;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102820; AAM51915.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14041 MW; C4195A821EEBB169 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 86
Q7SVG1
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ID Q7SVG1 PRELIMINARY; PRT; 117 AA.
AC Q7SVG1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=99NG732;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102823; AAM51918.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13960 MW; 9FC5F46458277DDB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 87
Q7SVF9
ID Q7SVF9 PRELIMINARY; PRT; 117 AA.
AC Q7SVF9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=99NG747;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102825; AAM51920.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14085 MW; 887D3F6DFEAA6E6 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 88
Q7SVF7
ID Q7SVF7 PRELIMINARY; PRT; 117 AA.
AC Q7SVF7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
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DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=99NG761;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102827; AAM51922.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14032 MW; 340A804D7684AADC CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 89
Q7SVF4
ID Q7SVF4 PRELIMINARY; PRT; 117 AA.
AC Q7SVF4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=99NG779;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102830; AAM51925.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14007 MW; CE92FDEF7CE1E03D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 90
Q7SVF3
ID Q7SVF3 PRELIMINARY; PRT; 117 AA.
AC Q7SVF3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
```

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GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG77;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102831; AAM51926.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14029 MW; 92B245BDB91467C6 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 91
Q7SVF2
ID Q7SVF2 PRELIMINARY; PRT; 117 AA.
AC Q7SVF2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG782;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102832; AAM51927.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13937 MW; C30B6DFEDF71B169 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 92
Q7SVE8
ID Q7SVE8 PRELIMINARY; PRT; 117 AA.
AC Q7SVE8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
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OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG859;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102836; AAM51931.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13989 MW; ABAOD93FB50BD88E CRC64;

Query Match          99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 93
Q7SVE7
ID Q7SVE7 PRELIMINARY; PRT; 117 AA.
AC Q7SVE7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG869;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102837; AAM51932.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14076 MW; E3B8E5D24354D5B3 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 94
Q7SVE4
ID Q7SVE4 PRELIMINARY; PRT; 117 AA.
AC Q7SVE4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=99NG901;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102841; AAM51936.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 14021 MW; 771766CAD25F3EE4 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 95
Q9E5R0
ID Q9E5R0 PRELIMINARY; PRT; 118 AA.
AC Q9E5R0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM19;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon.";
RL AIDS Res. Hum. Retroviruses 16:1319-1324 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM19;
RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemnji G.A., Eno L.T.,
RA Ngengasong J.N., Gao F., Rayfield M., Folks T.M., Pieniazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252111; AAG14320.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 14256 MW; CCCA2AF34D192690 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 118;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 96
Q90DJ5
ID Q90DJ5 PRELIMINARY; PRT; 121 AA.
AC Q90DJ5;
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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307736; AAL08797.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 14560 MW; C4601F79660B8C5D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 121;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 97
Q9EA94
ID Q9EA94 PRELIMINARY; PRT; 122 AA.
AC Q9EA94;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX513;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475 (2000).
DR EMBL; AF190958; AAG02320.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14674 MW; AFDA96E7701E7E5B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44
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Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 98

Q90DJ2

ID Q90DJ2 PRELIMINARY; PRT; 122 AA.

AC Q90DJ2;

DT 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=UG;

RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C., Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.; Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF307739; AAL08800.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.

DR Pfam; PF00517; GP41; 1.

DR Transmembrane.

KW

FT NON\_TER 1 1

FT NON\_TER 122 122

SQ SEQUENCE 122 AA; 14663 MW; AAC57DB097817188 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;

Best Local Similarity 96.2%; Pred. No. 1.9e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26

Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 99

Q9IJN0

ID Q9IJN0 PRELIMINARY; PRT; 122 AA.

AC Q9IJN0;

DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AR53;

RX MEDLINE=20346416; PubMed=10890362;

RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A., Baggs J., Lal R., Pieniazek D.;

RT "Evidence for a high frequency of HIV-1 subtype F infections among heterosexual population in Buenos Aries, Argentina.";

RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).

DR EMBL; AF220702; AAF76821.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.

DR Pfam; PF00517; GP41; 1.

DR Transmembrane.

KW

FT NON\_TER 1 1

FT NON\_TER 122 122

SQ SEQUENCE 122 AA; 14688 MW; 9C80D2BFEA0F3B35 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;

Best Local Similarity 96.2%; Pred. No. 1.9e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26

Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 100

Q9EA85

ID Q9EA85 PRELIMINARY; PRT; 122 AA.

AC Q9EA85;

DT 01-MAR-2001 (TReMBLrel. 16, Created)

DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BX84;

RX MEDLINE=20134570; PubMed=10669328;

RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P., Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;

RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic diversity in the United States.";

RT J. Infect. Dis. 181:470-475(2000).

RL EMBL; AF190967; AAG02329.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.

DR Pfam; PF00517; GP41; 1.

DR Transmembrane.

KW

FT NON\_TER 1 1

FT NON\_TER 122 122

SQ SEQUENCE 122 AA; 14692 MW; F777D665CE19C4E0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;

Best Local Similarity 96.2%; Pred. No. 1.9e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26

Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 101

Q9QIW8

ID Q9QIW8 PRELIMINARY; PRT; 122 AA.

AC Q9QIW8;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GP41ERRJ03;

RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R., Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A., Calazans A.R., Tanuri A.;

RT "Genotyping and phenotyping analysis of B and non-B Human immunodeficiency virus type 1 subtypes from patients under HAART.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF165536; AAF08481.1; -.

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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14708 MW; 4FP31B6E9075EE55 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db |:|||||
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 102
Q9QIW1 PRELIMINARY; PRT; 122 AA.
AC Q9QIW1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ10;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165543; AAF08488.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14733 MW; E2049BD5BAA9A6F0 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db |:|||||
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 103
Q9EA81 PRELIMINARY; PRT; 122 AA.
ID Q9EA81
AC Q9EA81;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=BX923;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190971; AAG02333.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14753 MW; C3FE4DB1F8B5BCBD CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db |:|||||
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 104
Q9YXQ0 PRELIMINARY; PRT; 122 AA.
ID Q9YXQ0
AC Q9YXQ0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP043;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034053; AAC79305.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14733 MW; B008FE9FF1F36D0C CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db |:|||||
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 105
Q9EAA4 PRELIMINARY; PRT; 122 AA.
ID Q9EAA4
AC Q9EAA4;
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DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BX157;  
RX MEDLINE=20134570; PubMed=10669328;  
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,  
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;  
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B  
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic  
RT diversity in the United States.";  
RL J. Infect. Dis. 181:470-475(2000).  
DR EMBL; AF190948; AAG02310.1; --.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14805 MW; D9C7A2283538108B CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44  
  
RESULT 106  
Q9QIW0 PRELIMINARY; PRT; 122 AA.  
AC Q9QIW0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GP41ERRJ11;  
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,  
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,  
RA Calazans A.R., Tanuri A.;  
RT "Genotyping and phenotyping analysis of B and non-B Human  
RT immunodeficiency virus type 1 subtypes from patients under HAART.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF165544; AAF08489.1; --.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14716 MW; CB39CE85DADE28FE CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44  
  
RESULT 107  
Q90DQ9 PRELIMINARY; PRT; 122 AA.  
ID Q90DQ9  
AC Q90DQ9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
RT and D infections in Uganda.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307672; AAL08733.1; --.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14684 MW; 52PF3DD5EC29032A CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44  
  
RESULT 108  
Q9IJN1 PRELIMINARY; PRT; 122 AA.  
ID Q9IJN1  
AC Q9IJN1;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR52;  
RX MEDLINE=20346416; PubMed=10890362;  
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,  
RA Baggs J., Lal R., Pieniazek D.;  
RT "Evidence for a high frequency of HIV-1 subtype F infections among  
RT heterosexual population in Buenos Aires, Argentina.";  
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).  
DR EMBL; AF220701; AAF76820.1; --.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.

KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14917 MW; 69477A001A80725D CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44  
  
RESULT 109  
Q90DK8 PRELIMINARY; PRT; 122 AA.  
AC Q90DK8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
RT and D infections in Uganda."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307723; AAL08784.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14779 MW; 9F2FF45071FBB1F9 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44  
  
RESULT 110  
Q90DS5 PRELIMINARY; PRT; 122 AA.  
AC Q90DS5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
RT and D infections in Uganda.";

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307656; AAL08717.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14713 MW; A6117281CEA10231 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44  
  
RESULT 111  
Q90DQ4 PRELIMINARY; PRT; 122 AA.  
AC Q90DQ4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
RT and D infections in Uganda.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307677; AAL08738.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14678 MW; 4C407CA763CC33F0 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44  
  
RESULT 112  
Q9EAA5 PRELIMINARY; PRT; 122 AA.  
AC Q9EAA5;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;



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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX126;
RX MEDLINE=20134570; PubMed=i0669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190947; AAG02309.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14859 MW; E6D2DAD15E71607A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 113
Q9IJM8
ID Q9IJM8 PRELIMINARY; PRT; 122 AA.
AC Q9IJM8;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220704; AAF76823.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14735 MW; 040891ADC152BEE4 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 114
Q9EAA2
ID Q9EAA2 PRELIMINARY; PRT; 122 AA.
AC Q9EAA2;
RX MEDLINE=20134570; PubMed=i0669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190947; AAG02309.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14859 MW; E6D2DAD15E71607A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44
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ID Q9EAA2 PRELIMINARY; PRT; 122 AA.
AC Q9EAA2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX161;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190950; AAG02312.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14751 MW; 302E5D7E45ED007D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 115
Q90DL1
ID Q90DL1 PRELIMINARY; PRT; 122 AA.
AC Q90DL1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307720; AAL08781.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14603 MW; 0937A2095F3DEFDE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
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Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 116  
Q90DS4  
ID Q90DS4 PRELIMINARY; PRT; 122 AA.  
AC Q90DS4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
and D infections in Uganda";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307657; AAL08718.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14748 MW; 2BF6CE35DF2E75A3 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 117  
Q9QIW3  
ID Q9QIW3 PRELIMINARY; PRT; 122 AA.  
AC Q9QIW3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GP41ERRJ08;  
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,  
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,  
RA Calazans A.R., Tanuri A.;  
RT "Genotyping and phenotyping analysis of B and non-B Human  
immunodeficiency virus type 1 subtypes from patients under HAART.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF165541; AAF08486.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.

DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14580 MW; 1D2451530391744E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 118  
Q90PX7  
ID Q90PX7 PRELIMINARY; PRT; 122 AA.  
AC Q90PX7;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TH35;  
RX MEDLINE=21270244; PubMed=11376043;  
RA Agwale S.M., Robbins K.E., Odama L., Saekhou A., Zeh C., Edubio A.,  
RA Njoku O.M., Sani-Gwarzo N., Gboun M.F., Gao F., Reitz M., Hone D.,  
RA Folks T.M., Pieniazek D., Wambebe C., Kalish M.L.;  
RT "Development of an env gp41-Based Heteroduplex Mobility Assay for  
Rapid Human Immunodeficiency Virus Type 1 Subtyping.";  
RL J. Clin. Microbiol. 39:2110-2114(2001).  
DR EMBL; AF343909; AAK66176.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14701 MW; 6A9C866990E66F1E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 119  
Q9QIV8  
ID Q9QIV8 PRELIMINARY; PRT; 122 AA.  
AC Q9QIV8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GP41ERRJ13;  
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,

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RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165546; AAF08491.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14794 MW; 63071E4A8FB3AB94 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 120
Q9WQZ1 ID Q9WQZ1 PRELIMINARY; PRT; 122 AA.
AC Q9WQZ1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TH27;
RA Pieniazek D., Yang C., Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113591; AAD42759.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14847 MW; 4E202AEC6B404A06 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 121
Q90PY1 ID Q90PY1 PRELIMINARY; PRT; 122 AA.
AC Q90PY1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
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OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97LB10;
RX MEDLINE=21270244; PubMed=11376043;
RA Agwale S.M., Robbins K.E., Odama L., Saekhou A., Zeh C., Edubio A.,
RA Njoku O.M., Sani-Gwarzo N., Gboun M.F., Gao F., Reitz M., Hone D.,
RA Folks T.M., Pieniazek D., Wambebe C., Kalish M.L.;
RT "Development of an env gp41-Based Heteroduplex Mobility Assay for
RT Rapid Human Immunodeficiency Virus Type 1 Subtyping.";
RL J. Clin. Microbiol. 39:2110-2114(2001).
DR EMBL; AF343905; AAK66172.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14329 MW; 8D3C10236D47593C CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 122
Q9ILL3 ID Q9ILL3 PRELIMINARY; PRT; 122 AA.
AC Q9ILL3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG1994;
RX MEDLINE=20284721; PubMed=10826488;
RA Downing R., Pieniazek D., Hu D.J., Biryahwaho B., Fridlund C.,
RA Rayfield M.A., Sempala S.D., Lal R.B.;
RT "Genetic characterization and phylogenetic analysis of HIV-1 subtype C
RT from Uganda.";
RL AIDS Res. Hum. Retroviruses 16:815-819(2000).
DR EMBL; AF206045; AAF82001.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14824 MW; 33645F96145A7B07 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RILAVERYLKDQQLGIWGCSGKLIC 44
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RESULT 123
Q90DN6
ID Q90DN6 PRELIMINARY; PRT; 122 AA.
AC Q90DN6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307695; AAL08756.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14728 MW; EEF439193281EDFE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 124
Q9QIV7
ID Q9QIV7 PRELIMINARY; PRT; 122 AA.
AC Q9QIV7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ14;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165547; AAF08492.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14764 MW; 3708166A0368F2A7 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 125
Q90DP5
ID Q90DP5 PRELIMINARY; PRT; 122 AA.
AC Q90DP5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307686; AAL08747.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14688 MW; EDA2A13E7C140E32 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 126
Q90DT0
ID Q90DT0 PRELIMINARY; PRT; 122 AA.
AC Q90DT0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307651; AAL08712.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
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DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14783 MW; BC2E81D16DFEAADF CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 127
Q9IJK5 PRELIMINARY; PRT; 122 AA.
AC Q9IJK5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR49;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aries, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220727; AAF76846.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14753 MW; 88DF5986C148B527 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 128
Q9YXN7 PRELIMINARY; PRT; 122 AA.
AC Q9YXN7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP093;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
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RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034066; AAC79318.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14759 MW; 26EB219834EBAE64 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 129
Q90DP0 PRELIMINARY; PRT; 122 AA.
AC Q90DP0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307691; AAL08752.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14718 MW; 97207DA663C5007B CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 130
Q9WQZ7 PRELIMINARY; PRT; 122 AA.
AC Q9WQZ7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
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OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CN37;
RA Pieniazek D., Yang C., Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113585; AAD42753.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14807 MW; 7744F5AF97830718 CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 122;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWCSGKLIC 44

RESULT 131
Q90DQ7
ID Q90DQ7 PRELIMINARY; PRT; 122 AA.
AC Q90DQ7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307674; AAL08735.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14740 MW; 33822EBC1A1A3ACE CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 122;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWCSGKLIC 44

RESULT 132
Q9ILK4
ID Q9ILK4 PRELIMINARY; PRT; 122 AA.
AC Q9ILK4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOZ36;
RX MEDLINE=20284721; PubMed=10826488;
RA Downing R., Pieniazek D., Hu D.J., Biryahwaho B., Fridlund C.,
RA Rayfield M.A., Sempala S.D., Lal R.B.;
RT "Genetic characterization and phylogenetic analysis of HIV-1 subtype C
RT from Uganda.";
RL AIDS Res. Hum. Retroviruses 16:815-819(2000).
DR EMBL; AF206054; AAF82010.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14771 MW; BCA91CA7B60ED207 CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 122;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLIC 26
Db 19 RILAIERYLKDQQLGIWCSGKLIC 44

RESULT 133
Q9YXN4
ID Q9YXN4 PRELIMINARY; PRT; 122 AA.
AC Q9YXN4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ97BRP116;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034069; AAC79321.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14811 MW; F154B211B9D456D5 CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 122;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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AC Q9ILK4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOZ36;
RX MEDLINE=20284721; PubMed=10826488;
RA Downing R., Pieniazek D., Hu D.J., Biryahwaho B., Fridlund C.,
RA Rayfield M.A., Sempala S.D., Lal R.B.;
RT "Genetic characterization and phylogenetic analysis of HIV-1 subtype C
RT from Uganda.";
RL AIDS Res. Hum. Retroviruses 16:815-819(2000).
DR EMBL; AF206054; AAF82010.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14771 MW; BCA91CA7B60ED207 CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 122;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLIC 26
Db 19 RILAIERYLKDQQLGIWCSGKLIC 44

RESULT 133
Q9YXN4
ID Q9YXN4 PRELIMINARY; PRT; 122 AA.
AC Q9YXN4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ97BRP116;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034069; AAC79321.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14811 MW; F154B211B9D456D5 CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 122;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 134  
Q9QIW7 PRELIMINARY; PRT; 122 AA.  
AC Q9QIW7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GP41ERRJ04;  
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,  
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,  
RA Calazans A.R., Tanuri A.;  
RT "Genotyping and phenotyping analysis of B and non-B Human  
immunodeficiency virus type 1 subtypes from patients under HAART."  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF165537; AAF08482.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14834 MW; 13711994A52A5B33 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 135  
Q9EA84 PRELIMINARY; PRT; 122 AA.  
AC Q9EA84;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BX88;  
RX MEDLINE=20134570; PubMed=10669328;  
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,  
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;  
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B  
subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic  
diversity in the United States."  
RL J. Infect. Dis. 181:470-475(2000).  
DR EMBL; AF190968; AAG02330.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.

DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14721 MW; 9F9F0AA594BD84B6 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 136  
Q9IJQ8 PRELIMINARY; PRT; 122 AA.  
AC Q9IJQ8;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR26;  
RX MEDLINE=20346416; PubMed=10890362;  
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,  
RA Baggs J., Lal R., Pieniazek D.;  
RT "Evidence for a high frequency of HIV-1 subtype F infections among  
heterosexual population in Buenos Aries, Argentina."  
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).  
DR EMBL; AF220674; AAF74226.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14733 MW; 89C6303ACD037238 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 137  
Q9YXR0 PRELIMINARY; PRT; 122 AA.  
AC Q9YXR0;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein immunodominant region (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RJ96BRP025;  
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,  
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,

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RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034043; AAC79295.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14795 MW; 313ED9A97E83167C CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 138
Q90DN0
ID Q90DN0 PRELIMINARY; PRT; 122 AA.
AC Q90DN0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Bityahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307701; AAL08762.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14712 MW; 960D670EAF51F06 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 139
Q9YXQ7
ID Q9YXQ7 PRELIMINARY; PRT; 122 AA.
AC Q9YXQ7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
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OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP030;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034046; AAC79298.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14635 MW; 906927994C59310A CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 140
Q9YXP9
ID Q9YXP9 PRELIMINARY; PRT; 122 AA.
AC Q9YXP9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP044;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034054; AAC79306.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14678 MW; A7C3D4FC2CE00A3D CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 141
Q90DI9
ID Q90DI9 PRELIMINARY; PRT; 122 AA.
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AC Q90DI9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307742; AAL08803.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14717 MW; 399CEE05F0C36976 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db |:|||||||||||||||||
19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 142
Q90DN2 ID Q90DN2 PRELIMINARY; PRT; 122 AA.
AC Q90DN2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307699; AAL08760.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14684 MW; 71EA72685F2915C3 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db |:|||||||||||||||||
19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 143
Q9YXR4 ID Q9YXR4 PRELIMINARY; PRT; 122 AA.
AC Q9YXR4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP009;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034039; AAC79291.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14739 MW; 40D4789EB8C888C2 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db |:|||||||||||||||||
19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 144
Q9IJQ7 ID Q9IJQ7 PRELIMINARY; PRT; 122 AA.
AC Q9IJQ7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR32;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR EMBL; AF220675; AAF74227.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14778 MW; DC8AE743D5815680 CRC64;
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AC Q90DI9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307742; AAL08803.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14717 MW; 399CEE05F0C36976 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db |:|||||||||||||||||
19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 142
Q90DN2 ID Q90DN2 PRELIMINARY; PRT; 122 AA.
AC Q90DN2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307699; AAL08760.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14684 MW; 71EA72685F2915C3 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db |:|||||||||||||||||
19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 143
Q9YXR4 ID Q9YXR4 PRELIMINARY; PRT; 122 AA.
AC Q9YXR4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP009;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034039; AAC79291.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14739 MW; 40D4789EB8C888C2 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db |:|||||||||||||||||
19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 144
Q9IJQ7 ID Q9IJQ7 PRELIMINARY; PRT; 122 AA.
AC Q9IJQ7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR32;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR EMBL; AF220675; AAF74227.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14778 MW; DC8AE743D5815680 CRC64;
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Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLLC 26  
Db 19 RVLAVERYLKDQQLGIWCSGKLLC 44

RESULT 145

Q9IJL2 PRELIMINARY; PRT; 122 AA.

AC Q9IJL2;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20346416; PubMed=10890362;  
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,  
RA Baggs J., Lal R., Pieniazek D.;  
RT "Evidence for a high frequency of HIV-1 subtype F infections among  
heterosexual population in Buenos Aires, Argentina.";  
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).  
DR EMBL; AF220720; AAF76839.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14755 MW; 0D30DB46BF54A8FA CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLLC 26  
Db 19 RVLAVERYLKDQQLGIWCSGKLLC 44

RESULT 146

Q90DR7 PRELIMINARY; PRT; 122 AA.

AC Q90DR7;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
and D infections in Uganda.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307664; AAL08725.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14693 MW; D20268AD4ADF8DEE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLLC 26  
Db 19 RVLAVERYLKDQQLGIWCSGKLLC 44

RESULT 147

Q90DR8 PRELIMINARY; PRT; 122 AA.

AC Q90DR8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
and D infections in Uganda.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307663; AAL08724.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14719 MW; 2DDC88CBD61B23B0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLLC 26  
Db 19 RVLAVERYLKDQQLGIWCSGKLLC 44

RESULT 148

Q9YXQ1 PRELIMINARY; PRT; 122 AA.

AC Q9YXQ1;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein immunodominant region (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RJ96BRP042;

RA	Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA	Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA	Rayfield M.;
RT	"HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF034052; AAC79304.1; -.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0019031; C:viral envelope; IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR000328; Env_GP41.
DR	Pfam; PF00517; GP41; 1.
KW	Transmembrane.
FT	NON_TER 1 1
FT	NON_TER 122 122
SQ	SEQUENCE 122 AA; 14792 MW; 7D5BB60146B8FD17 CRC64;
Query Match 99.3%; Score 138; DB 15; Length 122;	
Best Local Similarity 96.2%; Pred. No. 1.9e-13;	
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 RILAVERYLKDQQLGIWGCSGKLC 26
Db	19 RVLAVERYLKDQQLGIWGCSGKLC 44
:	
RESULT 149	
Q90DN9	PRELIMINARY; PRT; 122 AA.
AC	Q90DN9;
DT	01-DEC-2001 (TReMBLrel. 19, Created)
DT	01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE	Envelope glycoprotein (Fragment).
GN	ENV.
OS	Human immunodeficiency virus 1.
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX	NCBI_TaxID=11676;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=UG;
RA	Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA	Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT	"Similar distribution and continued predominance of HIV-1 subtypes A
RT	and D infections in Uganda.";
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF307692; AAL08753.1; -.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0019031; C:viral envelope; IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR000328; Env_GP41.
DR	Pfam; PF00517; GP41; 1.
KW	Transmembrane.
FT	NON_TER 1 1
FT	NON_TER 122 122
SQ	SEQUENCE 122 AA; 14814 MW; 151A3B6C2ED545E9 CRC64;
Query Match 99.3%; Score 138; DB 15; Length 122;	
Best Local Similarity 96.2%; Pred. No. 1.9e-13;	
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 RILAVERYLKDQQLGIWGCSGKLC 26
Db	19 RVLAVERYLKDQQLGIWGCSGKLC 44
:	
RESULT 150	
Q9QIV3	PRELIMINARY; PRT; 122 AA.
AC	Q9QIV3;
DT	01-MAY-2000 (TReMBLrel. 13, Created)
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE	Envelope glycoprotein (Fragment).

```
RESULT 152
Q9EA95
ID Q9EA95 PRELIMINARY; PRT; 122 AA.
AC Q9EA95;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX435;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190957; AAG02319.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14767 MW; 363549B0844EDEE5 CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 122;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 153
Q90DL7
ID Q90DL7 PRELIMINARY; PRT; 122 AA.
AC Q90DL7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307714; AAL08775.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14712 MW; 34B609D400C67CC5 CRC64;
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Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 122;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 154
Q90DQ8
ID Q90DQ8 PRELIMINARY; PRT; 122 AA.
AC Q90DQ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307673; AAL08734.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14693 MW; ED14B39C32BE0986 CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 122;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 155
Q90DJ1
ID Q90DJ1 PRELIMINARY; PRT; 122 AA.
AC Q90DJ1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307740; AAL08801.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
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DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14816 MW; 6BD0DF2301B4043A CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 156
Q9YXM8
ID Q9YXM8 PRELIMINARY; PRT; 122 AA.
AC Q9YXM8;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ97BRP132;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RA "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034075; AAC79327.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14571 MW; A5E7A49C0F1BA3AF CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 157
Q90DI8
ID Q90DI8 PRELIMINARY; PRT; 122 AA.
AC Q90DI8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AF307743; AAL08804.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14664 MW; 637EF68FDDC36A11 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 158
Q9IJN7
ID Q9IJN7 PRELIMINARY; PRT; 122 AA.
AC Q9IJN7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR33;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220695; AAF76814.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14704 MW; FDF3BD3C77B74A23 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 159
Q90DS6
ID Q90DS6 PRELIMINARY; PRT; 122 AA.
AC Q90DS6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
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RN
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307655; AAL08716.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14703 MW; 78DBC3BD63CE0776 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 160
Q90DP3
ID Q90DP3 PRELIMINARY; PRT; 122 AA.
AC Q90DP3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307688; AAL08749.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14818 MW; AC5D1E6C79749B83 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 161
Q90DK0
ID Q90DK0 PRELIMINARY; PRT; 122 AA.
AC Q90DK0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307731; AAL08792.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14742 MW; D4BE2130CDC37338 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 162
Q90DR3
ID Q90DR3 PRELIMINARY; PRT; 122 AA.
AC Q90DR3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307668; AAL08729.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14704 MW; FA86E5277AD367DC CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44
```

RESULT 163  
Q9IJN6 PRELIMINARY; PRT; 122 AA.  
AC Q9IJN6;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR34;  
RX MEDLINE=20346416; PubMed=10890362;  
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,  
RA Baggs J., Lal R., Pieniazek D.;  
RT "Evidence for a high frequency of HIV-1 subtype F infections among  
heterosexual population in Buenos Aires, Argentina.";  
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).  
DR EMBL; AF220696; AAF76815.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14718 MW; E822C25F0AAE61F1 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 164  
Q90DR2 PRELIMINARY; PRT; 122 AA.  
AC Q90DR2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
and D infections in Uganda.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307669; AAL08730.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14754 MW; 4A8A832E5D5488F2 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 165  
Q90DP8 PRELIMINARY; PRT; 122 AA.  
AC Q90DP8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
and D infections in Uganda.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307683; AAL08744.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14703 MW; 26D08CB693C40653 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 166  
Q9ILJ6 PRELIMINARY; PRT; 122 AA.  
AC Q9ILJ6;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ZIM29;  
RX MEDLINE=20284721; PubMed=10826488;  
RA Downing R., Pieniazek D., Hu D.J., Biryahwaho B., Fridlund C.,  
RA Rayfield M.A., Sempala S.D., Lal R.B.;  
RT "Genetic characterization and phylogenetic analysis of HIV-1 subtype C  
from Uganda.";  
RL AIDS Res. Hum. Retroviruses 16:815-819(2000).  
DR EMBL; AF206062; AAF82018.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.

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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14746 MW; 194509B404DDC61B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44
|:|||||

RESULT 167
Q9IJP6 PRELIMINARY; PRT; 122 AA.
AC Q9IJP6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR15;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aries, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR EMBL; AF220686; AAF74238.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14729 MW; D1CF7E2498427841 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44
|:|||||

RESULT 168
Q9EA88 PRELIMINARY; PRT; 122 AA.
AC Q9EA88;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=BX797;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475 (2000).
DR EMBL; AF190964; AAG02326.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14661 MW; 11024C717439B83A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44
|:|||||

RESULT 169
Q90DS1 PRELIMINARY; PRT; 122 AA.
AC Q90DS1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307660; AAL08721.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14727 MW; 63657CA763C369EF CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44
|:|||||

RESULT 170
Q9IJQ6 PRELIMINARY; PRT; 122 AA.
ID Q9IJQ6
AC Q9IJQ6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR35;  
RX MEDLINE=20346416; PubMed=10890362;  
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,  
RA Baggs J., Lal R., Pieniazek D.;  
RT "Evidence for a high frequency of HIV-1 subtype F infections among  
RT heterosexual population in Buenos Aries, Argentina.";  
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).  
DR EMBL; AF220676; AAF74228.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14844 MW; DCB555869433C0EF CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCSGKLIC 26  
|:|||||||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWCSGKLIC 44  
|:|||||||||||||||||||||  
  
RESULT 171  
Q9IJQ5 PRELIMINARY; PRT; 122 AA.  
AC Q9IJQ5;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR38;  
RX MEDLINE=20346416; PubMed=10890362;  
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,  
RA Baggs J., Lal R., Pieniazek D.;  
RT "Evidence for a high frequency of HIV-1 subtype F infections among  
RT heterosexual population in Buenos Aries, Argentina.";  
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).  
DR EMBL; AF220677; AAF74229.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14841 MW; 6752EF2965DD4709 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCSGKLIC 26  
|:|||||||||||||||||||||

Db 19 RVLAVERYLKDQQLGIWCSGKLIC 44  
|:|||||||||||||||||||||  
  
RESULT 172  
Q90DK2 PRELIMINARY; PRT; 122 AA.  
AC Q90DK2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
RT and D infections in Uganda.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307729; AAL08790.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14668 MW; 9AB027886DFBEA73 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCSGKLIC 26  
|:|||||||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWCSGKLIC 44  
|:|||||||||||||||||||||  
  
RESULT 173  
Q90DN1 PRELIMINARY; PRT; 122 AA.  
AC Q90DN1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
RT and D infections in Uganda.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307700; AAL08761.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122

SQ SEQUENCE 122 AA; 14684 MW; AEBB7D3AE1B0BE23 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 174  
Q90DM2

ID Q90DM2 PRELIMINARY; PRT; 122 AA.  
AC Q90DM2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
RT and D infections in Uganda."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307709; AAL08770.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14797 MW; 70078BACAF37931 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 175  
Q90DN3

ID Q90DN3 PRELIMINARY; PRT; 122 AA.  
AC Q90DN3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
RT and D infections in Uganda."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307698; AAL08759.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14848 MW; FEF3F75550D01A63 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 176  
Q91JP2

ID Q91JP2 PRELIMINARY; PRT; 122 AA.  
AC Q91JP2;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR22;  
RX MEDLINE=20346416; PubMed=10890362;  
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,  
RA Baggs J., Lal R., Pieniazek D.;  
RT "Evidence for a high frequency of HIV-1 subtype F infections among  
RT heterosexual population in Buenos Aires, Argentina."  
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).  
DR EMBL; AF220690; AAF76809.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14748 MW; 61E64BEC3F42460A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 177  
Q90DS7

ID Q90DS7 PRELIMINARY; PRT; 122 AA.  
AC Q90DS7;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.

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RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307654; AAL08715.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14861 MW; CE141BESAF77D68C CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 178
Q9QIU7 PRELIMINARY; PRT; 122 AA.
ID Q9QIU7
AC Q9QIU7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ24;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165557; AAF08502.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14635 MW; D052E4B73AE3008E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 179
Q9IJQ1 PRELIMINARY; PRT; 122 AA.
ID Q9IJQ1
AC Q9IJQ1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR59;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR EMBL; AF220681; AAF74233.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14676 MW; D2B27F903F4EB2AD CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 180
Q9WR01 PRELIMINARY; PRT; 122 AA.
ID Q9WR01
AC Q9WR01;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97ug398;
RA Pieniazek D., Yang C., Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113581; AAD42749.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14848 MW; PEF3F75550D01A63 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44
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RESULT 181  
Q9IJL1  
ID Q9IJL1 PRELIMINARY; PRT; 122 AA.  
AC Q9IJL1;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR47;  
RX MEDLINE=20346416; PubMed=10890362;  
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,  
RA Baggs J., Lal R., Pieniazek D.;  
RT "Evidence for a high frequency of HIV-1 subtype F infections among  
heterosexual population in Buenos Aries, Argentina.";  
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).  
DR EMBL; AF220721; AAF76840.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14778 MW; 81C07541D00E8C39 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
|:|||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 182  
Q9IJM9  
ID Q9IJM9 PRELIMINARY; PRT; 122 AA.  
AC Q9IJM9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR60;  
RX MEDLINE=20346416; PubMed=10890362;  
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,  
RA Baggs J., Lal R., Pieniazek D.;  
RT "Evidence for a high frequency of HIV-1 subtype F infections among  
heterosexual population in Buenos Aries, Argentina.";  
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).  
DR EMBL; AF220703; AAF76822.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14679 MW; ABE4BB421A98FFA5 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
|:|||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 183  
Q9IJQ9  
ID Q9IJQ9 PRELIMINARY; PRT; 122 AA.  
AC Q9IJQ9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR20;  
RX MEDLINE=20346416; PubMed=10890362;  
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,  
RA Baggs J., Lal R., Pieniazek D.;  
RT "Evidence for a high frequency of HIV-1 subtype F infections among  
heterosexual population in Buenos Aries, Argentina.";  
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).  
DR EMBL; AF220673; AAF74225.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14757 MW; C342A2EBE4725B3E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
|:|||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 184  
Q9IJP5  
ID Q9IJP5 PRELIMINARY; PRT; 122 AA.  
AC Q9IJP5;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR17;  
RX MEDLINE=20346416; PubMed=10890362;  
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,  
RA Baggs J., Lal R., Pieniazek D.;  
RT "Evidence for a high frequency of HIV-1 subtype F infections among  
heterosexual population in Buenos Aries, Argentina.";  
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).  
DR EMBL; AF220687; AAF76806.1; -.



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DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14749 MW; 810E603A372AA8C4 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
   |:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44
   |:|||||

RESULT 185
Q9ILM2 PRELIMINARY; PRT; 122 AA.
AC Q9ILM2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG275;
RX MEDLINE=20284721; PubMed=10826488;
RA Downing R., Pieniazek D., Hu D.J., Biryahwaho B., Fridlund C.,
RA Rayfield M.A., Sempala S.D., Lal R.B.;
RT "Genetic characterization and phylogenetic analysis of HIV-1 subtype C
from Uganda.";
RL AIDS Res. Hum. Retroviruses 16:815-819(2000).
DR EMBL; AF206036; AAF81992.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14768 MW; DED3A42C9DF76D38 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
   |:|||||
Db 19 RILAIERYLKDQQLGIWGCSGKLIC 44
   |:|||||

RESULT 186
Q90DT2 PRELIMINARY; PRT; 122 AA.
AC Q90DT2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307649; AAL08710.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14713 MW; A6117281CEA10231 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
   |:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44
   |:|||||

RESULT 187
Q9YXP3 PRELIMINARY; PRT; 122 AA.
AC Q9YXP3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP071;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034060; AAC79312.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14701 MW; 4EED351A06F7C74F CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
   |:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44
   |:|||||

RESULT 188
Q9EA82 PRELIMINARY; PRT; 122 AA.
AC Q9EA82;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BK922;  
RX MEDLINE=20134570; PubMed=10669328;  
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,  
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;  
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B  
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic  
RT diversity in the United States.";  
RL J. Infect. Dis. 181:470-475(2000).  
DR EMBL; AF190970; AAG02332.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14804 MW; CF6AF2DC9EDA9C69 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSKLIC 26  
|:|||||||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWCGSKLIC 44  
  
RESULT 189  
Q90DK7 PRELIMINARY; PRT; 122 AA.  
AC Q90DK7;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
RT and D infections in Uganda.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307724; AAL08785.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14750 MW; 10D65E3EF7D41A9E CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSKLIC 26  
|:|||||||||||||||||||||

Db 19 RVLAVERYLKDQQLGIWCGSKLIC 44  
  
RESULT 190  
Q9IJQ4 PRELIMINARY; PRT; 122 AA.  
AC Q9IJQ4;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR39;  
RX MEDLINE=20346416; PubMed=10890362;  
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,  
RA Baggs J., Lal R., Pieniazek D.;  
RT "Evidence for a high frequency of HIV-1 subtype F infections among  
RT heterosexual population in Buenos Aries, Argentina.";  
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).  
DR EMBL; AF220678; AAF74230.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14703 MW; 834721661D3A360E CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSKLIC 26  
|:|||||||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWCGSKLIC 44  
  
RESULT 191  
Q90DM3 PRELIMINARY; PRT; 122 AA.  
AC Q90DM3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
RT and D infections in Uganda.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307708; AAL08769.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122

SQ SEQUENCE 122 AA; 14603 MW; 3DDFA4A8CEC96CB7 CRC64;  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44  
RESULT 192  
Q90DL6 PRELIMINARY; PRT; 122 AA.  
AC Q90DL6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
and D infections in Uganda."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307715; AAL08776.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14779 MW; BF277FAFE662C99F CRC64;  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44  
RESULT 193  
Q9WQZ4 PRELIMINARY; PRT; 122 AA.  
AC Q9WQZ4;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GH3;  
RA Pieniazek D., Yang C., Lal R.L.;  
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O  
isolates provides an alternate region for subtype determination."  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF113588; AAD42756.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14857 MW; 1FC64594F75A207C CRC64;  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44  
RESULT 194  
Q9YXN5 PRELIMINARY; PRT; 122 AA.  
AC Q9YXN5;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein immunodominant region (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RJ97BRPI05;  
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,  
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,  
RA Rayfield M.;  
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF034068; AAC79320.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 14845 MW; EC2A71B0086440C3 CRC64;  
Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44  
RESULT 195  
Q9QIU8 PRELIMINARY; PRT; 122 AA.  
AC Q9QIU8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GP41ERRJ23;  
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,

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RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165556; AAF08501.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14733 MW; 91CD821BA7A7FFCB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 196
Q90DN8
ID Q90DN8 PRELIMINARY; PRT; 122 AA.
AC Q90DN8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307693; AAL08754.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14719 MW; B1A827E231D3748D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 197
Q90DN5
ID Q90DN5 PRELIMINARY; PRT; 122 AA.
AC Q90DN5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
```

```
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307696; AAL08757.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14738 MW; 28669DBD00E3693E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 198
Q9IJP7
ID Q9IJP7 PRELIMINARY; PRT; 122 AA.
AC Q9IJP7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR11;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aries, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR EMBL; AF220685; AAF74237.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14704 MW; 5538AD9D2B012589 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44
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RESULT 199
Q90DL2
ID Q90DL2 PRELIMINARY; PRT; 122 AA.
AC Q90DL2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund.C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307719; AAL08780.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14662 MW; 86300081CAC9AA3A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred.No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 200
Q7ZJS6
ID Q7ZJS6 PRELIMINARY; PRT; 122 AA.
AC Q7ZJS6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG95-327;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M
RT (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol
RT integrase, and env gp41.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214083; AAO61803.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14748 MW; 68F4BCCA8DC1DBC0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred.No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 200
Q7ZJS6
ID Q7ZJS6 PRELIMINARY; PRT; 122 AA.
AC Q7ZJS6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG95-327;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M
RT (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol
RT integrase, and env gp41.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214083; AAO61803.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14748 MW; 68F4BCCA8DC1DBC0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred.No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 200
Q7ZJS1
ID Q7ZJS1 PRELIMINARY; PRT; 122 AA.
AC Q7ZJS1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BK132;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M
RT (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol
RT integrase, and env gp41.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214088; AAO61808.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14675 MW; 4E83B592C7C10ACB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred.No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 202
Q7ZJS1
ID Q7ZJS1 PRELIMINARY; PRT; 122 AA.
AC Q7ZJS1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BK132;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M
RT (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol
RT integrase, and env gp41.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214088; AAO61808.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14675 MW; 4E83B592C7C10ACB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred.No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44
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QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 201
Q7ZJS2
ID Q7ZJS2 PRELIMINARY; PRT; 122 AA.
AC Q7ZJS2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG95-422;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M
RT (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol
RT integrase, and env gp41.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214087; AAO61807.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14675 MW; 4E83B592C7C10ACB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred.No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 202
Q7ZJS1
ID Q7ZJS1 PRELIMINARY; PRT; 122 AA.
AC Q7ZJS1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BK132;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M
RT (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol
RT integrase, and env gp41.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214088; AAO61808.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14675 MW; 4E83B592C7C10ACB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred.No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44
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SQ SEQUENCE 122 AA; 14674 MW; 95E8C3532B34165F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

Db

RESULT 203  
Q7ZJSO

ID Q7ZJSO PRELIMINARY; PRT; 122 AA.

AC Q7ZJSO;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BZ167;

RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;

RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41.";

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY214089; AAC61809.1;

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.

DR Pfam; PF00517; GP41; 1.

KW Envelope protein.

FT NON\_TER 1

FT NON\_TER 122

SQ SEQUENCE 122 AA; 14759 MW; 9548FEAC44CD741E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

Db

RESULT 204  
Q7ZJR8

ID Q7ZJR8 PRELIMINARY; PRT; 122 AA.

AC Q7ZJR8;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TH1600;

RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;

RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41.";

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY214091; AAC61811.1;

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.

DR Pfam; PF00517; GP41; 1.

KW Envelope protein.

FT NON\_TER 1

FT NON\_TER 122

SQ SEQUENCE 122 AA; 14786 MW; 6C4FAFF8579F9104 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

Db

RESULT 205  
Q7ZJR7

ID Q7ZJR7 PRELIMINARY; PRT; 122 AA.

AC Q7ZJR7;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=US1;

RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;

RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41.";

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY214092; AAC61812.1;

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.

DR Pfam; PF00517; GP41; 1.

KW Envelope protein.

FT NON\_TER 1

FT NON\_TER 122

SQ SEQUENCE 122 AA; 14748 MW; 08FF40E09139D71E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

Db

RESULT 206  
Q7ZJR6

ID Q7ZJR6 PRELIMINARY; PRT; 122 AA.

AC Q7ZJR6;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=US2;

RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;

RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol

RT integrase, and env gp41.";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY214093; AA061813.1; -;  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14767 MW; 038D675003BEC8A5 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 207

Q7ZJR5 ID Q7ZJR5 PRELIMINARY; PRT; 122 AA.  
AC Q7ZJR5;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=US3;  
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;  
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41.";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY214094; AA061814.1; -;  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14822 MW; 3732E22879944B0D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 208

Q7ZJP0 ID Q7ZJP0 PRELIMINARY; PRT; 122 AA.  
AC Q7ZJP0;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=IVCO3671;  
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;  
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41.";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY214119; AA061839.1; -;  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14762 MW; 7272AD069B69B89 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 209

Q8J3S ID Q8J3S PRELIMINARY; PRT; 123 AA.  
AC Q8J3S;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,  
RA de Sousa G., Canas-Ferreira W.;  
RT "Molecular epidemiology of HIV-1 infection in Portugal: high prevalence of non-B subtypes.";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ318398; CAC85977.1; -;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 123  
SQ SEQUENCE 123 AA; 14914 MW; C94786EC61260642 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 123;  
Best Local Similarity 96.2%; Pred. No. 1.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 17 RVLAVERYLKDQQLGIWCGSGKLC 42

RESULT 210

Q8J3R5 ID Q8J3R5 PRELIMINARY; PRT; 123 AA.  
AC Q8J3R5;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 (Fragment).

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GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA de Sousa A., Parreira R., Venenno T., Franco M., Piedade J.,
RA "Molecular epidemiology of HIV-1 infection in Portugal: high
RT prevalence of non-B subtypes.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ318406; CAC85985.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 123
SQ SEQUENCE 123 AA; 14897 MW; 5D37383E8DCEE8E0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 123;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 17 RVLAVERYLKDQQLGIWGCSGKLC 42

RESULT 211
QYXR3 PRELIMINARY; PRT; 123 AA.
AC QYXR3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP011;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034040; AAC79292.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 123
SQ SEQUENCE 123 AA; 14791 MW; D79184FA768C0E60 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 123;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 212
Q8J3S2 PRELIMINARY; PRT; 123 AA.
AC Q8J3S2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,
RA de Sousa G., Canas-Ferreira W.;
RT "Molecular epidemiology of HIV-1 infection in Portugal: high
RT prevalence of non-B subtypes.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ318399; CAC85978.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 123
SQ SEQUENCE 123 AA; 14862 MW; 0F1E4342A90F42C9 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 123;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 17 RVLAVERYLKDQQLGIWGCSGKLC 42

RESULT 213
Q8AEX1 PRELIMINARY; PRT; 123 AA.
AC Q8AEX1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,
RA Germano de Sousa J., Canas-Ferreira W.;
RT "Genetic diversity of HIV-1 spreading among intravenous drug users in
RT Lisbon, Portugal.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ429042; CAD23678.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 123
SQ SEQUENCE 123 AA; 14883 MW; 17C6F08AB45DFEFA CRC64;

Query Match 99.3%; Score 138; DB 15; Length 123;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 17 RVLAVERYLKDQQLGIWGCSGKLC 42
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ID Q8J3S2 PRELIMINARY; PRT; 123 AA.
AC Q8J3S2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,
RA de Sousa G., Canas-Ferreira W.;
RT "Molecular epidemiology of HIV-1 infection in Portugal: high
RT prevalence of non-B subtypes.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ318399; CAC85978.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 123
SQ SEQUENCE 123 AA; 14862 MW; 0F1E4342A90F42C9 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 123;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 17 RVLAVERYLKDQQLGIWGCSGKLC 42

RESULT 213
Q8AEX1 PRELIMINARY; PRT; 123 AA.
AC Q8AEX1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,
RA Germano de Sousa J., Canas-Ferreira W.;
RT "Genetic diversity of HIV-1 spreading among intravenous drug users in
RT Lisbon, Portugal.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ429042; CAD23678.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 123
SQ SEQUENCE 123 AA; 14883 MW; 17C6F08AB45DFEFA CRC64;

Query Match 99.3%; Score 138; DB 15; Length 123;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 17 RVLAVERYLKDQQLGIWGCSGKLC 42
```



RESULT 214  
Q8J3R7  
ID Q8J3R7 PRELIMINARY; PRT; 124 AA.  
AC Q8J3R7;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,  
RA de Sousa G., Canas-Ferreira W.;  
RT "Molecular epidemiology of HIV-1 infection in Portugal: high  
RT prevalence of non-B subtypes.";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ318404; CAC85983.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 124 124  
SQ SEQUENCE 124 AA; 14833 MW; 1373000B4D608F5A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 124;  
Best Local Similarity 96.2%; Pred. No. 2e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 18 RVLAVERYLKDQQLGIWGCSGKLIC 43

RESULT 215  
Q9YZ03  
ID Q9YZ03 PRELIMINARY; PRT; 124 AA.  
AC Q9YZ03;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=140.223;  
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,  
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;  
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in  
RT Uganda.";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF006866; AAD01310.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 124 124  
SQ SEQUENCE 124 AA; 14820 MW; 37C85D6A080B393B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 124;  
Best Local Similarity 96.2%; Pred. No. 2e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 24 RVLAVERYLKDQQLGIWGCSGKLIC 49

RESULT 216  
Q9IWP9  
ID Q9IWP9 PRELIMINARY; PRT; 125 AA.  
AC Q9IWP9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=85CD244;  
RX MEDLINE=21134754; PubMed=11242522;  
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,  
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;  
RT "Predominance of HIV type 1 subtype G among commercial sex workers  
RT from Kinshasa, Democratic Republic of Congo.";  
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).  
DR EMBL; AF260477; AAF71944.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 125 125  
SQ SEQUENCE 125 AA; 14805 MW; 4EB9BF1C23F33469 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 125;  
Best Local Similarity 96.2%; Pred. No. 2e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 33 RVLAVERYLKDQQLGIWGCSGKLIC 58

RESULT 217  
Q9IWQ9  
ID Q9IWQ9 PRELIMINARY; PRT; 126 AA.  
AC Q9IWQ9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=85CD116;  
RX MEDLINE=21134754; PubMed=11242522;  
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,  
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;  
RT "Predominance of HIV type 1 subtype G among commercial sex workers  
RT from Kinshasa, Democratic Republic of Congo.";  
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).  
DR EMBL; AF260467; AAF71934.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.

```
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 15246 MW; A73CDFAAECC6E129 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 126;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 17 RVLAVERYLKDQQLGIWGCSGKLIC 42

RESULT 218
Q9YXX6 PRELIMINARY; PRT; 127 AA.
AC Q9YXX6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=264.643;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF006923; AAD01367.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 127 127
SQ SEQUENCE 127 AA; 15335 MW; A3422CAD00B2CFB7 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 127;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 25 RVLAVERYLKDQQLGIWGCSGKLIC 50

RESULT 219
Q9IWR0 PRELIMINARY; PRT; 127 AA.
AC Q9IWR0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD085;
RX MEDLINE=21134754; PubMed=11242522;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
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RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
RT "Predominance of HIV type 1 subtype G among commercial sex workers
RT from Kinshasa, Democratic Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL; AF260466; AAF71933.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 127 127
SQ SEQUENCE 127 AA; 15272 MW; 076E4A6CBABE822E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 127;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 220
Q9WM82 PRELIMINARY; PRT; 127 AA.
AC Q9WM82;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=122.335;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF006846; AAD01290.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 127 127
SQ SEQUENCE 127 AA; 15296 MW; 6F8361B317E554CA CRC64;

Query Match 99.3%; Score 138; DB 15; Length 127;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 25 RVLAVERYLKDQQLGIWGCSGKLIC 50

RESULT 221
Q9WM85 PRELIMINARY; PRT; 127 AA.
AC Q9WM85;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
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OS Human immunodeficiency virus 1.
OC Viruses; Retrovid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=102.938;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006839; AAD01283.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 127
FT NON_TER 127
SQ SEQUENCE 127 AA; 15243 MW; 325EDBCD3C504556 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 127;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
   |:|||||||||||||||||||||
Db 25 RVLAVERYLKDQQLGIWGCSGKLIC 50

RESULT 222
Q9YYW8 PRELIMINARY; PRT; 127 AA.
AC Q9YYW8
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=326.642;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006937; AAD01381.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 127
FT NON_TER 127
SQ SEQUENCE 127 AA; 15215 MW; A3C1DEB0CB5DCE00 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 127;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
   |:|||||||||||||||||||||
Db 25 RVLAVERYLKDQQLGIWGCSGKLIC 50

RESULT 223
Q9IHY1 PRELIMINARY; PRT; 128 AA.
AC Q9IHY1
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98CM010;
RX MEDLINE=20386754; PubMed=10933623;
RA Yang C., Gao F., Fonjungo P.N., Zekeng L., van der Groen G.,
RA Pieniazek D., Schable C., Lal R.B.;
RT "Phylogenetic analysis of protease and transmembrane regions of HIV
RT type 1 group O.";
RL AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
DR EMBL; AF229203; AAF71457.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 128
FT NON_TER 128
SQ SEQUENCE 128 AA; 15459 MW; B04136F4362EF827 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 128;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
   |:|||||||||||||||||||||
Db 25 RVLAVERYLKDQQLGIWGCSGKLIC 50

RESULT 224
Q9YYZ0 PRELIMINARY; PRT; 129 AA.
AC Q9YYZ0
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=225.318;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006898; AAD01342.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 129
FT NON_TER 129
SQ SEQUENCE 129 AA; 15523 MW; 433A3AF534C73CD7 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 129;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
FT NON\_TER 1  
FT NON\_TER 130  
SQ SEQUENCE 130 AA; 15662 MW; 33C9EE30DA2A98C4 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 130;  
Best Local Similarity 96.2%; Pred. No. 2e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 20 RVLAVERYLKDQQLGIWGCSGKLIC 45

RESULT 225  
Q9YYV2 PRELIMINARY; PRT; 129 AA.  
AC Q9YYV2;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=230.298;  
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,  
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;  
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in  
RT Uganda";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF006912; AAD01356.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 129  
SQ SEQUENCE 129 AA; 15469 MW; 3B952B1A2D229808 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 129;  
Best Local Similarity 96.2%; Pred. No. 2e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 26 RVLAVERYLKDQQLGIWGCSGKLIC 51

RESULT 226  
Q9IWR6 PRELIMINARY; PRT; 130 AA.  
AC Q9IWR6;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=85CD246;  
RX MEDLINE=21134754; PubMed=11242522;  
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,  
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;  
RT "Predominance of HIV type 1 subtype G among commercial sex workers  
RT from Kinshasa, Democratic Republic of Congo";  
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).  
DR EMBL; AF260460; AAF71927.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.

KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 130  
SQ SEQUENCE 130 AA; 15662 MW; 33C9EE30DA2A98C4 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 130;  
Best Local Similarity 96.2%; Pred. No. 2.1e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 20 RVLAVERYLKDQQLGIWGCSGKLIC 45

RESULT 227  
Q9YYW6 PRELIMINARY; PRT; 130 AA.  
AC Q9YYW6;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=326.662;  
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,  
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;  
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in  
RT Uganda";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF006941; AAD01385.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 130  
SQ SEQUENCE 130 AA; 15581 MW; 7652D93F692D2527 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 130;  
Best Local Similarity 96.2%; Pred. No. 2.1e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 27 RVLAVERYLKDQQLGIWGCSGKLIC 52

RESULT 228  
Q9IWW0 PRELIMINARY; PRT; 132 AA.  
AC Q9IWW0;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=85CD225;  
RX MEDLINE=21134754; PubMed=11242522;  
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,  
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;  
RT "Predominance of HIV type 1 subtype G among commercial sex workers



```
RT from Kinshasa, Democratic Republic of Congo." ;
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL; AF260476; AAF71943.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 132
FT NON_TER 133
SQ SEQUENCE 132 AA; 15607 MW; 6A05003B8A9F2B14 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 132;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 35 RVLAVERYLKDQQLGIWGCSGKLIC 60
|:|||||

RESULT 229
Q8UQZ6 PRELIMINARY; PRT; 133 AA.
AC Q8UQZ6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=00ZM148F;
RX MEDLINE=21602569; PubMed=11739704;
RA Trask S.A., Derdeyn C.A., Fideli U., Chen Y., Meleth S., Kasolo F.,
RA Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
transmission in a heterosexual cohort of discordant couples in
Zambia." ;
RT J. Virol. 76:397-405(2002).
RL J. Virol. 76:397-405(2002).
DR EMBL; AF405152; AAL66672.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 16145 MW; 6DBD34C92AFDA77D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 27 RVLAVERYLKDQQLGIWGCSGKLIC 52
|:|||||

RESULT 230
Q8UQW8 PRELIMINARY; PRT; 133 AA.
AC Q8UQW8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=00ZM148F;
RX MEDLINE=21602569; PubMed=11739704;
RA Trask S.A., Derdeyn C.A., Fideli U., Chen Y., Meleth S., Kasolo F.,
RA Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
transmission in a heterosexual cohort of discordant couples in
Zambia." ;
RT J. Virol. 76:397-405(2002).
RL J. Virol. 76:397-405(2002).
DR EMBL; AF405152; AAL66672.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 16145 MW; 6DBD34C92AFDA77D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 27 RVLAVERYLKDQQLGIWGCSGKLIC 52
|:|||||

RESULT 230
Q8UQW8 PRELIMINARY; PRT; 133 AA.
AC Q8UQW8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=127.568;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
Uganda." ;
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006850; AAD01294.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 15931 MW; 184000DE060C81 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98ZM098M;
RX MEDLINE=21602569; PubMed=11739704;
RA Trask S.A., Derdeyn C.A., Fideli U., Chen Y., Meleth S., Kasolo F.,
RA Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
transmission in a heterosexual cohort of discordant couples in
Zambia." ;
RT J. Virol. 76:397-405(2002).
RL J. Virol. 76:397-405(2002).
DR EMBL; AF405187; AAL66700.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 15827 MW; 5AD3D0BAA789780B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 27 RVLAVERYLKDQQLGIWGCSGKLIC 52
|:|||||

RESULT 231
Q9YZ13 PRELIMINARY; PRT; 133 AA.
AC Q9YZ13;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=127.568;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
Uganda." ;
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006850; AAD01294.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 15931 MW; 184000DE060C81 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 29 RVLAVERYLKDQQLGIWGCSGKLIC 54
|:|||||
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RESULT 232
Q90Q18
ID Q90Q18 PRELIMINARY; PRT; 133 AA.
AC Q90Q18;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MO1557;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331123; AAK92334.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 15612 MW; 84142CA9E98813E6 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 36 RVLAVERYLKDQQLGIWGCSGKLC 61

RESULT 233
Q90Q57
ID Q90Q57 PRELIMINARY; PRT; 133 AA.
AC Q90Q57;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MO1475;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331084; AAK92295.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 15765 MW; 8534092BDE8ADB4F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
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Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 36 RVLAVERYLKDQQLGIWGCSGKLC 61

RESULT 234
Q90Q63
ID Q90Q63 PRELIMINARY; PRT; 133 AA.
AC Q90Q63;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MO1468;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331078; AAK92289.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 15774 MW; 8F84BF80B2EF26F8 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 36 RVLAVERYLKDQQLGIWGCSGKLC 61

RESULT 235
Q90PZ3
ID Q90PZ3 PRELIMINARY; PRT; 133 AA.
AC Q90PZ3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MO1617;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331148; AAK92359.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
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KW Transmembrane. 1  
FT NON\_TER 133  
FT NON\_TER 133  
SQ SEQUENCE 133 AA; 15648 MW; 13A163CF35C3D6F2 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 133;  
Best Local Similarity 96.2%; Pred. No. 2.1e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 36 RVLAVERYLKDQQLGIWCGSGKLC 61  
  
RESULT 236  
Q90Q37  
ID Q90Q37 PRELIMINARY; PRT; 133 AA.  
AC Q90Q37;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=99ES-MOI517;  
RX MEDLINE=21322034; PubMed=11429126;  
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,  
RA Garcia-Saiz A.;  
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea."  
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).  
DR EMBL; AF331104; AAK92315.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 133  
SQ SEQUENCE 133 AA; 15775 MW; 8DED10B25057F953 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 133;  
Best Local Similarity 96.2%; Pred. No. 2.1e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 36 RVLAVERYLKDQQLGIWCGSGKLC 61  
  
RESULT 237  
Q8UQZ4  
ID Q8UQZ4 PRELIMINARY; PRT; 133 AA.  
AC Q8UQZ4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=98ZM043M;  
RX MEDLINE=21602569; PubMed=11739704;  
RA Trask S.A., Derdeyn C.A., Fideli U., Chen Y., Meleth S., Kasolo F.,  
RA Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;  
RT "Molecular epidemiology of human immunodeficiency virus type 1

RT transmission in a heterosexual cohort of discordant couples in  
RT Zambia.";  
RL J. Virol. 76:397-405(2002).  
DR EMBL; AF405154; AAL66674.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 133  
SQ SEQUENCE 133 AA; 16057 MW; 6650D8E2480703B0 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 133;  
Best Local Similarity 96.2%; Pred. No. 2.1e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 27 RVLAVERYLKDQQLGIWCGSGKLC 52  
  
RESULT 238  
Q90Q25  
ID Q90Q25 PRELIMINARY; PRT; 133 AA.  
AC Q90Q25;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=99ES-MOI541;  
RX MEDLINE=21322034; PubMed=11429126;  
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,  
RA Garcia-Saiz A.;  
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea."  
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).  
DR EMBL; AF331116; AAK92327.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 133  
SQ SEQUENCE 133 AA; 15821 MW; D62443B42FE9EA93 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 133;  
Best Local Similarity 96.2%; Pred. No. 2.1e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 36 RVLAVERYLKDQQLGIWCGSGKLC 61  
  
RESULT 239  
Q8UQZ3  
ID Q8UQZ3 PRELIMINARY; PRT; 133 AA.  
AC Q8UQZ3;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.

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OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97ZM043F;
RX MEDLINE=21602569; PubMed=11739704;
RA Trask S.A., Derdeyn C.A., Fidelis U., Chen Y., Meleth S., Kasolo F.,
RA Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
RT transmission in a heterosexual cohort of discordant couples in
RT Zambia.";
RL J. Virol. 76:397-405(2002).
DR EMBL; AF405155; AAL66675.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 16058 MW; 665E360246E9E3B0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db [1]
27 RVLAVERYLKDQQLGIWGCSGKLC 52

RESULT 240
Q9IWR3 PRELIMINARY; PRT; 133 AA.
AC Q9IWR3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD300;
RX MEDLINE=21134754; PubMed=11242522;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
RT "Predominance of HIV type 1 subtype G among commercial sex workers
RT from Kinshasa, Democratic Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL; AF260463; AAF71930.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 16036 MW; 60554BC9E396A823 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db [1]
24 RILAVERYLKDQQLGIWGCSGKLC 49
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RESULT 241
Q90Q27 PRELIMINARY; PRT; 133 AA.
AC Q90Q27;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MO1536;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331114; AAK92325.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 15658 MW; 200E088E3482A65A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db [1]
36 RVLAVERYLKDQQLGIWGCSGKLC 61

RESULT 242
Q90Q35 PRELIMINARY; PRT; 133 AA.
AC Q90Q35;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MO1521;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331106; AAK92317.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 15794 MW; 9426B9B28EA26F6F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
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Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 36 RVLAVERYLKDQQLGIWGCSGKLIC 61

RESULT 243

Q9IWQ6 PRELIMINARY; PRT; 134 AA.

AC Q9IWQ6;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=85CD260;  
RX MEDLINE=21134754; PubMed=11242522;  
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,  
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;  
RT "Predominance of HIV type 1 subtype G among commercial sex workers  
from Kinshasa, Democratic Republic of Congo.";  
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).  
DR EMBL; AF260470; AAF71937.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 134 134  
SQ SEQUENCE 134 AA; 15361 MW; EA6E5DFE360A0322 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 134;  
Best Local Similarity 96.2%; Pred. No. 2.1e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 34 RVLAVERYLKDQQLGIWGCSGKLIC 59

RESULT 244

Q8UQZ5 PRELIMINARY; PRT; 136 AA.

AC Q8UQZ5;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=00ZM148M;  
RX MEDLINE=21602569; PubMed=11739704;  
RA Trask S.A., Derdeyn C.A., Fideli U., Chen Y., Meleth S., Kasolo F.,  
RA Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;  
RT "Molecular epidemiology of human immunodeficiency virus type 1  
transmission in a heterosexual cohort of discordant couples in  
Zambia.";  
RL J. Virol. 76:397-405(2002).  
DR EMBL; AF405153; AAL66673.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 136 136  
SQ SEQUENCE 136 AA; 16415 MW; EF1069F332CF8128 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 136;  
Best Local Similarity 96.2%; Pred. No. 2.2e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 24 RVLAVERYLKDQQLGIWGCSGKLIC 49

RESULT 245

Q9DQM0 PRELIMINARY; PRT; 137 AA.

AC Q9DQM0;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SP-M1270;  
RX MEDLINE=20584646; PubMed=11153079;  
RA Ortiz M., Munoz L., Bernal A., Rodriguez A., Zorraquino A.,  
RA Vellido J., Salas A., Moreno A., Garcia-Saiz A.;  
RT "Molecular Characterization of Non-B HIV Type 1 Subtypes from Africa  
in Spain.";  
RL AIDS Res. Hum. Retroviruses 16:1967-1971(2000).  
DR EMBL; AF255938; AAG36893.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 137 137  
SQ SEQUENCE 137 AA; 16458 MW; 94CED7A1B23984C1 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 137;  
Best Local Similarity 96.2%; Pred. No. 2.2e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 35 RVLAVERYLKDQQLGIWGCSGKLIC 60

RESULT 246

Q7SLZ5 PRELIMINARY; PRT; 139 AA.

AC Q7SLZ5;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GT853;

RA Gonzalez Perez M.P., Garcia Saiz A.;  
RT "Epidemiological and molecular characteristics of HIV and HTLV  
infection in Equatorial Guinea, 1996-1998."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF530021; AAF87752.1; --  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 139  
SQ SEQUENCE 139 AA; 16799 MW; C94B96DEBAB9658C CRC64;

Query Match 99.3%; Score 138; DB 15; Length 139;  
Best Local Similarity 96.2%; Pred. No. 2.2e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLIC 26  
|:|||||  
Db 37 RVLAVERYLKDQQLGIWCSGKLIC 62

RESULT 247  
Q7SM28

ID Q7SM28 PRELIMINARY; PRT; 140 AA.  
AC Q7SM28;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GM577;  
RA Gonzalez Perez M.P., Garcia Saiz A.;  
RT "Epidemiological and molecular characteristics of HIV and HTLV  
infection in Equatorial Guinea, 1996-1998."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF529988; AAP87719.1; --  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 140  
SQ SEQUENCE 140 AA; 16660 MW; 486490EA23F36A6A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 140;  
Best Local Similarity 96.2%; Pred. No. 2.2e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLIC 26  
|:|||||  
Db 37 RVLAVERYLKDQQLGIWCSGKLIC 62

RESULT 248

Q9IWQ1  
ID Q9IWQ1 PRELIMINARY; PRT; 143 AA.  
AC Q9IWQ1;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=85CD350;  
RX MEDLINE=21134754; PubMed=11242522;  
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,  
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;  
RT "Predominance of HIV type 1 subtype G among commercial sex workers  
from Kinshasa, Democratic Republic of Congo.";

RL AIDS Res. Hum. Retroviruses 17:361-365(2001).  
DR EMBL; AF260475; AAF71942.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 143  
SQ SEQUENCE 143 AA; 17160 MW; D8157A905740B24E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 143;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLIC 26  
|:|||||  
Db 35 RVLAVERYLKDQQLGIWCSGKLIC 60

RESULT 249

Q9IWP3  
ID Q9IWP3 PRELIMINARY; PRT; 144 AA.  
AC Q9IWP3;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=85CD299;  
RX MEDLINE=21134754; PubMed=11242522;  
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,  
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;  
RT "Predominance of HIV type 1 subtype G among commercial sex workers  
from Kinshasa, Democratic Republic of Congo.";  
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).  
DR EMBL; AF260483; AAF71950.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 144  
SQ SEQUENCE 144 AA; 17098 MW; 2D21BB1C3390CC29 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLIC 26  
|:|||||  
Db 35 RVLAVERYLKDQQLGIWCSGKLIC 60

RESULT 250  
Q70207

ID Q70207 PRELIMINARY; PRT; 144 AA.  
AC Q70207;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein gp41 region (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

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OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PBLPD;
RX MEDLINE=95251923; PubMed=7734184;
RA Calabro M.L., Zanolto C., Calderazzo F., Crivellaro C., Del Mistro A.,
RA De Rossi A., Chieco-Bianchi L.;
RT "HIV-1 infection of the thymus: evidence for a cytopathic and
RT thymotropic viral variant in vivo.";
RL AIDS Res. Hum. Retroviruses 11:11-19(1995).
DR EMBL; U09253; AAA79039.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 17229 MW; 4B2F7347E3E65C4A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|:|||||
Db 34 RVLAVERYLKDQQLGIWGCSGKLC 59

RESULT 251
Q70206
ID Q70206 PRELIMINARY; PRT; 144 AA.
AC Q70206;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=THYPD;
RX MEDLINE=95251923; PubMed=7734184;
RA Calabro M.L., Zanolto C., Calderazzo F., Crivellaro C., Del Mistro A.,
RA De Rossi A., Chieco-Bianchi L.;
RT "HIV-1 infection of the thymus: evidence for a cytopathic and
RT thymotropic viral variant in vivo.";
RL AIDS Res. Hum. Retroviruses 11:11-19(1995).
DR EMBL; U09252; AAA79038.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 17227 MW; 233F7297E0E12C5B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|:|||||
Db 34 RVLAVERYLKDQQLGIWGCSGKLC 59

RESULT 252
Q7ZCE9
ID Q7ZCE9 PRELIMINARY; PRT; 144 AA.
AC Q7ZCE9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX46-2;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185371; AA065646.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16863 MW; 7213537CD404BDEB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|:|||||
Db 50 RVLAVERYLKDQQLGIWGCSGKLC 75

RESULT 253
Q7ZCE2
ID Q7ZCE2 PRELIMINARY; PRT; 144 AA.
AC Q7ZCE2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX50-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185378; AA065653.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16770 MW; C3A3781F5BF13207 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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ID Q7ZCE9 PRELIMINARY; PRT; 144 AA.
AC Q7ZCE9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX46-2;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185371; AA065646.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16863 MW; 7213537CD404BDEB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|:|||||
Db 50 RVLAVERYLKDQQLGIWGCSGKLC 75

RESULT 253
Q7ZCE2
ID Q7ZCE2 PRELIMINARY; PRT; 144 AA.
AC Q7ZCE2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX50-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185378; AA065653.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16770 MW; C3A3781F5BF13207 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
SQ SEQUENCE 144 AA; 16795 MW; 5970F4D602702384 CRC64;  
Db 50 RVLAVERYLKDQQLGIWGCSGKLIC 75  
RESULT 254  
Q7ZCE1 PRELIMINARY; PRT; 144 AA.  
ID Q7ZCE1  
AC Q7ZCE1;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLJX50-2;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185379; AA065654.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16872 MW; 94E89EC614E2B3FE CRC64;  
Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 50 RVLAVERYLKDQQLGIWGCSGKLIC 75  
RESULT 255  
Q7ZCE0 PRELIMINARY; PRT; 144 AA.  
ID Q7ZCE0  
AC Q7ZCE0;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLJX51-1;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185380; AA065655.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16872 MW; 94E89EC614E2B3FE CRC64;  
Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 50 RVLAVERYLKDQQLGIWGCSGKLIC 75  
RESULT 256  
Q7ZCD8 PRELIMINARY; PRT; 144 AA.  
ID Q7ZCD8  
AC Q7ZCD8;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLJX52-2;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185382; AA065657.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16795 MW; 23E382827E63D165 CRC64;  
Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 50 RVLAVERYLKDQQLGIWGCSGKLIC 75  
RESULT 257  
Q7ZCC6 PRELIMINARY; PRT; 144 AA.  
ID Q7ZCC6  
AC Q7ZCC6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLJX59-1;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16795 MW; 5970F4D602702384 CRC64;  
Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 50 RVLAVERYLKDQQLGIWGCSGKLIC 75  
RESULT 256  
Q7ZCD8 PRELIMINARY; PRT; 144 AA.  
ID Q7ZCD8  
AC Q7ZCD8;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLJX52-2;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185382; AA065657.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16795 MW; 23E382827E63D165 CRC64;  
Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 50 RVLAVERYLKDQQLGIWGCSGKLIC 75  
RESULT 257  
Q7ZCC6 PRELIMINARY; PRT; 144 AA.  
ID Q7ZCC6  
AC Q7ZCC6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLJX59-1;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.



DR EMBL; AY185394; AAC65669.1; --  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR Pfam; PF00517; GP41; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 FT NON\_TER 144  
 SQ SEQUENCE 144 AA; 16777 MW; 616A253A437E1613 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;  
 Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
 Db 50 RVLAVERYLKDQQLGIWCGSGKLC 75

RESULT 258  
 Q7ZCC5 PRELIMINARY; PRT; 144 AA.

ID Q7ZCC5  
 AC Q7ZCC5;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HRLUX59-2;  
 RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
 RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
 RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
 RT 20) resistance in enfuvirtide-naïve patients infected with subtype B  
 RT and non-B HIV-1.";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY185395; AAC65670.1; --  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR Pfam; PF00517; GP41; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 FT NON\_TER 144  
 SQ SEQUENCE 144 AA; 16814 MW; 7BF4060DD37E0D7F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;  
 Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
 Db 50 RVLAVERYLKDQQLGIWCGSGKLC 75

RESULT 259  
 Q7ZCC2 PRELIMINARY; PRT; 144 AA.

ID Q7ZCC2  
 AC Q7ZCC2;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

Query Match 99.3%; Score 138; DB 15; Length 144;  
 Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
 Db 50 RVLAVERYLKDQQLGIWCGSGKLC 75

RESULT 258  
 Q7ZCC5 PRELIMINARY; PRT; 144 AA.

ID Q7ZCC5  
 AC Q7ZCC5;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=HRLUX61-2;  
 RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
 RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
 RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
 RT 20) resistance in enfuvirtide-naïve patients infected with subtype B  
 RT and non-B HIV-1.";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY185398; AAC65673.1; --  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR Pfam; PF00517; GP41; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 FT NON\_TER 144  
 SQ SEQUENCE 144 AA; 16897 MW; 74B5617D37F7468 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;  
 Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
 Db 50 RVLAVERYLKDQQLGIWCGSGKLC 75

RESULT 260  
 Q7ZCB9 PRELIMINARY; PRT; 144 AA.

ID Q7ZCB9  
 AC Q7ZCB9;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HRLUX63-1;  
 RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
 RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
 RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
 RT 20) resistance in enfuvirtide-naïve patients infected with subtype B  
 RT and non-B HIV-1.";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY185401; AAC65676.1; --  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR Pfam; PF00517; GP41; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 FT NON\_TER 144  
 SQ SEQUENCE 144 AA; 16861 MW; 50C5BF2735E767C CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;  
 Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
 Db 50 RVLAVERYLKDQQLGIWCGSGKLC 75

RESULT 261  
 Q7ZCB8 PRELIMINARY; PRT; 144 AA.

ID Q7ZCB8  
 AC Q7ZCB8;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

Query Match 99.3%; Score 138; DB 15; Length 144;  
 Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
 Db 50 RVLAVERYLKDQQLGIWCGSGKLC 75

RESULT 261  
 Q7ZCB8 PRELIMINARY; PRT; 144 AA.

ID Q7ZCB8  
 AC Q7ZCB8;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

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DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX63-2;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185402; AA065677.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16951 MW; 99940DA637DA9D7F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db 50 RVLAVERYLKDQQLGIWCSGKLC 75

RESULT 262
Q7ZCB5
ID Q7ZCB5 PRELIMINARY; PRT; 144 AA.
AC Q7ZCB5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX65-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185405; AA065680.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16937 MW; 68F2D1D36DBF781B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db 50 RVLAVERYLKDQQLGIWCSGKLC 75
```

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RESULT 263
Q7ZCB4
ID Q7ZCB4 PRELIMINARY; PRT; 144 AA.
AC Q7ZCB4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX65-2;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185406; AA065681.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16938 MW; 68FF6ABED6DF781B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db 50 RVLAVERYLKDQQLGIWCSGKLC 75

RESULT 264
Q7ZCB1
ID Q7ZCB1 PRELIMINARY; PRT; 144 AA.
AC Q7ZCB1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX67-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185409; AA065684.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16904 MW; C4E289C330AA4F41 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
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Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16701 MW; 40PFEFCF6BBF14F4 CRC64;

Db 50 RVLAVERYLKDQQLGIWGCSGKLIC 75

Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 265

Q7ZCB0 ID Q7ZCB0 PRELIMINARY; PRT; 144 AA.  
AC Q7ZCB0;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX67-2;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185410; AAC65685.1; --.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16904 MW; C4E289C330AA4F41 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16904 MW; C4E289C330AA4F41 CRC64;

Db 50 RVLAVERYLKDQQLGIWGCSGKLIC 75

Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 266

Q7ZCA6 ID Q7ZCA6 PRELIMINARY; PRT; 144 AA.  
AC Q7ZCA6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX70-1;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185414; AAC65689.1; --.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.

KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16701 MW; 40PFEFCF6BBF14F4 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16701 MW; 40PFEFCF6BBF14F4 CRC64;

Db 50 RVLAVERYLKDQQLGIWGCSGKLIC 75

Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 267

Q7ZCA5 ID Q7ZCA5 PRELIMINARY; PRT; 144 AA.  
AC Q7ZCA5;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX70-2;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185415; AAC65690.1; --.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16706 MW; 10D841FB587B9ECC CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16706 MW; 10D841FB587B9ECC CRC64;

Db 50 RVLAVERYLKDQQLGIWGCSGKLIC 75

Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 268

Q7ZC98 ID Q7ZC98 PRELIMINARY; PRT; 144 AA.  
AC Q7ZC98;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX74-1;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B

RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185422; AA065697.1; -;  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 144  
SQ SEQUENCE 144 AA; 16833 MW; 0FB4031FCB7D4BCE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 50 RVLAVERYLKDQQLGIWGCSGKLC 75

RESULT 269  
Q7ZC96 PRELIMINARY; PRT; 144 AA.  
ID Q7ZC96  
AC Q7ZC96;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

SEQUENCE FROM N.A.  
RC STRAIN=HRLUX75-1;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185424; AA065699.1; -;  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 144  
SQ SEQUENCE 144 AA; 16877 MW; 619841A2A7D5ECD4 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 50 RVLAVERYLKDQQLGIWGCSGKLC 75

RESULT 270  
Q7ZC95 PRELIMINARY; PRT; 144 AA.  
ID Q7ZC95  
AC Q7ZC95;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX75-2;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185425; AA065700.1; -;  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 144  
SQ SEQUENCE 144 AA; 16856 MW; E89941A2A9E2F16C CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 50 RVLAVERYLKDQQLGIWGCSGKLC 75

RESULT 271  
Q7ZC71 PRELIMINARY; PRT; 144 AA.  
ID Q7ZC71  
AC Q7ZC71;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

SEQUENCE FROM N.A.  
RC STRAIN=HRLUX89-1;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185449; AA065724.1; -;  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 144  
SQ SEQUENCE 144 AA; 16824 MW; F1EBA0FCC4691895 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 50 RVLAVERYLKDQQLGIWGCSGKLC 75

RESULT 272  
Q7ZC70 PRELIMINARY; PRT; 144 AA.  
ID Q7ZC70  
AC Q7ZC70;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)



DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX89-2;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.  
RL EMBL; AY185450; AAC65725.1; --  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 16810 MW; E811A60B17491895 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db |:||||| 144 144  
50 RVLAVERYLKDQQLGIWCGSGKLC 75

RESULT 273  
Q7ZC66 PRELIMINARY; PRT; 145 AA.

AC Q7ZC66;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX4;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B  
RT subtype HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.  
RL EMBL; AY185454; AAC65729.1; --  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 145 145  
SQ SEQUENCE 145 AA; 16911 MW; AF6C707A2076B6DE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 145;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db |:||||| 145 145  
48 RVLAVERYLKDQQLGIWCGSGKLC 73

RESULT 274  
Q7ZC49 PRELIMINARY; PRT; 145 AA.

AC Q7ZC49;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX31;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B  
RT subtype HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.  
RL EMBL; AY185454; AAC65729.1; --  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 145 145  
SQ SEQUENCE 145 AA; 16911 MW; AF6C707A2076B6DE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 145;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db |:||||| 145 145  
48 RVLAVERYLKDQQLGIWCGSGKLC 73

RESULT 275  
Q7ZC39 PRELIMINARY; PRT; 145 AA.

AC Q7ZC39;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX31;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B  
RT subtype HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.  
RL EMBL; AY185481; AAC65756.1; --  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 145 145  
SQ SEQUENCE 145 AA; 17033 MW; F899F94713F5D4D0 CRC64;

RESULT 274  
Q7ZC49 PRELIMINARY; PRT; 145 AA.

AC Q7ZC49;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX21;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B  
RT subtype HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.  
RL EMBL; AY185471; AAC65746.1; --  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 145 145  
SQ SEQUENCE 145 AA; 17036 MW; FA30B782F065B72D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 145;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db |:||||| 145 145  
48 RVLAVERYLKDQQLGIWCGSGKLC 73

RESULT 275  
Q7ZC39 PRELIMINARY; PRT; 145 AA.

AC Q7ZC39;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX31;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B  
RT subtype HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.  
RL EMBL; AY185481; AAC65756.1; --  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 145 145  
SQ SEQUENCE 145 AA; 17033 MW; F899F94713F5D4D0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 145;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db |:||||| 145 145  
48 RVLAVERYLKDQQLGIWCGSGKLC 73

RESULT 275  
Q7ZC39 PRELIMINARY; PRT; 145 AA.

AC Q7ZC39;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX31;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B  
RT subtype HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.  
RL EMBL; AY185481; AAC65756.1; --  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 145 145  
SQ SEQUENCE 145 AA; 17033 MW; F899F94713F5D4D0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 145;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db |:||||| 145 145  
48 RVLAVERYLKDQQLGIWCGSGKLC 73

RESULT 275  
Q7ZC39 PRELIMINARY; PRT; 145 AA.

AC Q7ZC39;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX31;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B  
RT subtype HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.  
RL EMBL; AY185481; AAC65756.1; --  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 145 145  
SQ SEQUENCE 145 AA; 17033 MW; F899F94713F5D4D0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 145;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 48 RVLAVERYLKDQQLGIWGCSGKLIC 73

RESULT 276  
Q7ZC33  
ID Q7ZC33 PRELIMINARY; PRT; 145 AA.  
AC Q7ZC33;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX37;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B  
RT subtype HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBBJ databases.  
DR EMBL; AY185487; AA065762.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 145  
FT NON\_TER 145 145  
SQ SEQUENCE 145 AA; 16912 MW; F4BBFB6175BD662D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 145;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 48 RVLAVERYLKDQQLGIWGCSGKLIC 73

RESULT 277  
Q7ZC32  
ID Q7ZC32 PRELIMINARY; PRT; 145 AA.  
AC Q7ZC32;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX38;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B  
RT subtype HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBBJ databases.  
DR EMBL; AY185488; AA065763.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 145  
FT NON\_TER 145 145  
SQ SEQUENCE 145 AA; 17043 MW; 4487A149CEC57570 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 145;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 48 RVLAVERYLKDQQLGIWGCSGKLIC 73

RESULT 278  
Q7ZC68  
ID Q7ZC68 PRELIMINARY; PRT; 146 AA.  
AC Q7ZC68;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX2;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B  
RT subtype HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBBJ databases.  
DR EMBL; AY185452; AA065727.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 146  
FT NON\_TER 146 146  
SQ SEQUENCE 146 AA; 17151 MW; 70D3C7E584C9DA3A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 146;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 48 RVLAVERYLKDQQLGIWGCSGKLIC 73

RESULT 279  
Q7ZC30  
ID Q7ZC30 PRELIMINARY; PRT; 146 AA.  
AC Q7ZC30;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HRLUX40;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;

RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B  
RT subtype HIV-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY185490; AA065765.1; --  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 146  
SQ SEQUENCE 146 AA; 17107 MW; 61C2B7806FD99929 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 146;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 48 RVLAVERYLKDQQLGIWGCSGKLIC 73  
  
RESULT 280  
Q7SM37  
ID Q7SM37 PRELIMINARY; PRT; 146 AA.  
AC Q7SM37;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GM142;  
RA Gonzalez Perez M.P., Garcia Saiz A.;  
RT "Epidemiological and molecular characteristics of HIV and HTLV  
RT infection in Equatorial Guinea, 1996-1998.";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF529979; AAP87710.1; --  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 146  
SQ SEQUENCE 146 AA; 17542 MW; AC94EDD0C3829CD1 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 146;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 37 RVLAVERYLKDQQLGIWGCSGKLIC 62  
  
RESULT 281  
Q7SM44  
ID Q7SM44 PRELIMINARY; PRT; 147 AA.  
AC Q7SM44;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GI280;  
RA Gonzalez Perez M.P., Garcia Saiz A.;

RT "Epidemiological and molecular characteristics of HIV and HTLV  
RT infection in Equatorial Guinea, 1996-1998.";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF529972; AAP87703.1; --  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 147  
SQ SEQUENCE 147 AA; 17548 MW; 8F5E56215D1D1682 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 147;  
Best Local Similarity 96.2%; Pred. No. 2.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 37 RVLAVERYLKDQQLGIWGCSGKLIC 62  
  
RESULT 282  
Q8J3N3  
ID Q8J3N3 PRELIMINARY; PRT; 155 AA.  
AC Q8J3N3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 protein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22092513; PubMed=12097573;  
RA Boutonnet N., Janssens W., Boutton C., Verschelde J.L., Heyndrickx L.,  
RA Beirnaert E., van der Groen G., Lasters I.;  
RT "Comparison of predicted scaffold-compatible sequence variation in the  
RT triple-hairpin structure of human immunodeficiency virus type 1 gp41  
RT with patient data.";  
RL J. Virol. 76:7595-7606 (2002).  
DR EMBL; AJ428020; CAD20972.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR00328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 155  
FT NON\_TER 155  
SQ SEQUENCE 155 AA; 18372 MW; DA6CFB7A42286226 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 155;  
Best Local Similarity 96.2%; Pred. No. 2.5e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 35 RVLAVERYLKDQQLGIWGCSGKLIC 60  
  
RESULT 283  
Q8J3Q1  
ID Q8J3Q1 PRELIMINARY; PRT; 155 AA.  
AC Q8J3Q1;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 protein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22092513; PubMed=12097573;

RA Boutonnet N., Janssens W., Boutton C., Verschelde J.L., Heyndrickx L.,  
RA Beirnaert E., van der Groen G., Lasters I.,  
RT "Comparison of predicted scaffold-compatible sequence variation in the  
RT triple-hairpin structure of human immunodeficiency virus type 1 gp41  
RT with patient data.";  
RL J. Virol. 76:7595-7606 (2002).  
DR EMBL; AJ428002; CAD20954.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 155 155  
SQ SEQUENCE 155 AA; 18273 MW; B4EBAC6F0C278B2F CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 155;  
Best Local Similarity 96.2%; Pred. No. 2.5e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 35 RVLAVERYLKDQQLGIWGCSGKLIC 60  
  
RESULT 284  
Q8JAL7 ID Q8JAL7 PRELIMINARY; PRT; 156 AA.  
AC Q8JAL7;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=95BRRJ014;  
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,  
RA Morgado M.G.;  
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian  
RT Southeastern and Southern regions.";  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF463427; AAM90803.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 156 156  
SQ SEQUENCE 156 AA; 17855 MW; 21F22059FB9A919B CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 156;  
Best Local Similarity 96.2%; Pred. No. 2.5e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 55 RVLAVERYLKDQQLGIWGCSGKLIC 80  
  
RESULT 285  
Q8J3Q9 ID Q8J3Q9 PRELIMINARY; PRT; 156 AA.  
AC Q8J3Q9;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 protein (Fragment).

GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22092513; PubMed=12097573;  
RA Boutonnet N., Janssens W., Boutton C., Verschelde J.L., Heyndrickx L.,  
RA Beirnaert E., van der Groen G., Lasters I.,  
RT "Comparison of predicted scaffold-compatible sequence variation in the  
RT triple-hairpin structure of human immunodeficiency virus type 1 gp41  
RT with patient data.";  
RL J. Virol. 76:7595-7606 (2002).  
DR EMBL; AJ427994; CAD20946.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 156 156  
SQ SEQUENCE 156 AA; 18491 MW; 54BFB80BC6FB76DD CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 156;  
Best Local Similarity 96.2%; Pred. No. 2.5e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 35 RVLAVERYLKDQQLGIWGCSGKLIC 60  
  
RESULT 286  
Q90E80 ID Q90E80 PRELIMINARY; PRT; 163 AA.  
AC Q90E80;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SC15;  
RA Feng H., Huang Y., Yang D., Tang H., Hu X.,  
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from  
RT Sichuan.";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY037950; AAK72323.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 163 163  
SQ SEQUENCE 163 AA; 19242 MW; C580C6B44534772E CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 163;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 51 RVLAVERYLKDQQLGIWGCSGKLIC 76  
  
RESULT 287  
Q90E76



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ID Q90E76 PRELIMINARY; PRT; 163 AA.
AC Q90E76;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC27;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RT Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037954; AAK72327.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19285 MW; 289917C07613D1FE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 51 RILAVERYLKDQQLGIWGCSGKLIC 76

RESULT 288
Q90E69 PRELIMINARY; PRT; 163 AA.
AC Q90E69;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC22;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RT Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037961; AAK72334.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19200 MW; EF4E811ED3871087 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 51 RILAVERYLKDQQLGIWGCSGKLIC 76

RESULT 289
Q90E73 PRELIMINARY; PRT; 163 AA.
AC Q90E73;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC03;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RT Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037957; AAK72330.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19274 MW; 121FACDABCD75A0D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 51 RILAVERYLKDQQLGIWGCSGKLIC 76

RESULT 290
Q90E67 PRELIMINARY; PRT; 163 AA.
AC Q90E67;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC23;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RT Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037963; AAK72336.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19200 MW; EF4E811ED3871087 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 51 RILAVERYLKDQQLGIWGCSGKLIC 76
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Db 51 RILAVERYLKDQQLGIWGCSGKLIC 76

RESULT 289
Q90E73 PRELIMINARY; PRT; 163 AA.
ID Q90E73
AC Q90E73;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC03;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RT Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037957; AAK72330.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19274 MW; 121FACDABCD75A0D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 51 RILAVERYLKDQQLGIWGCSGKLIC 76

RESULT 290
Q90E67 PRELIMINARY; PRT; 163 AA.
ID Q90E67
AC Q90E67;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC23;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RT Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037963; AAK72336.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19200 MW; EF4E811ED3871087 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 51 RILAVERYLKDQQLGIWGCSGKLIC 76
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Best Local Similarity 96.2%; Pred. No. 2.6e-13; -  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 51 RVLAVERYLKDQQLGIWGCSGKLIC 76

RESULT 291

Q90E68  
ID Q90E68 PRELIMINARY; PRT; 163 AA.  
AC Q90E68;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SC26;  
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;  
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from Sichuan."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY037962; AAK72335.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 163  
SQ SEQUENCE 163 AA; 19200 MW; EF4E811ED3871087 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 51 RVLAVERYLKDQQLGIWGCSGKLIC 76

RESULT 292

Q90E71  
ID Q90E71 PRELIMINARY; PRT; 163 AA.  
AC Q90E71;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SC19;  
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;  
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from Sichuan."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY037959; AAK72332.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.

Query Match 99.3%; Score 138; DB 15; Length 163;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 51 RVLAVERYLKDQQLGIWGCSGKLIC 76

FT NON\_TER 1  
FT NON\_TER 163  
SQ SEQUENCE 163 AA; 19311 MW; F325C8FD7143D237 CRC64;  
Query Match 99.3%; Score 138; DB 15; Length 163;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 51 RVLAVERYLKDQQLGIWGCSGKLIC 76

RESULT 293

Q90E74  
ID Q90E74 PRELIMINARY; PRT; 163 AA.  
AC Q90E74;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SC18;  
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;  
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from Sichuan."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY037956; AAK72329.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 163  
SQ SEQUENCE 163 AA; 19347 MW; C397B8EE5624A725 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 51 RVLAVERYLKDQQLGIWGCSGKLIC 76

RESULT 294

Q90E72  
ID Q90E72 PRELIMINARY; PRT; 163 AA.  
AC Q90E72;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SC24;  
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;  
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from Sichuan."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY037958; AAK72331.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.

Query Match 99.3%; Score 138; DB 15; Length 163;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 51 RVLAVERYLKDQQLGIWGCSGKLIC 76

DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 163 163  
SQ SEQUENCE 163 AA; 19370 MW; 82180C09173ADCA8 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 163;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db 51 RVLAVERYLKDQQLGIWGCSGKLC 76  
  
RESULT 295  
Q90E65 ID Q90E65 PRELIMINARY; PRT; 163 AA.  
AC Q90E65;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SC05;  
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;  
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from Sichuan."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY037965; AAK72338.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 163 163  
SQ SEQUENCE 163 AA; 19324 MW; ED9E3D98EC3DFE74 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 163;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db 51 RVLAVERYLKDQQLGIWGCSGKLC 76  
  
RESULT 296  
Q8J3R2 ID Q8J3R2 PRELIMINARY; PRT; 164 AA.  
AC Q8J3R2;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 protein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22092513; PubMed=12097573;  
RA Boutonnet N., Janssens W., Boutton C., Verschelde J.L., Heyndrickx L.,

RA Beirnaert E., van der Groen G., Lasters I.;  
RT "Comparison of predicted scaffold-compatible sequence variation in the triple-hairpin structure of human immunodeficiency virus type 1 gp41 with patient data."  
RL J. Virol. 76:7595-7606 (2002).  
DR EMBL; AJ427991; CAD20943.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 164 164  
SQ SEQUENCE 164 AA; 19291 MW; F91298D132E359C7 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 164;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db 44 RVLAVERYLKDQQLGIWGCSGKLC 69  
  
RESULT 297  
Q90E78 ID Q90E78 PRELIMINARY; PRT; 164 AA.  
AC Q90E78;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SC13;  
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;  
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from Sichuan."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY037952; AAK72325.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 164 164  
SQ SEQUENCE 164 AA; 19224 MW; 078AD292ED08AC4F CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 164;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db 52 RVLAVERYLKDQQLGIWGCSGKLC 77  
  
RESULT 298  
Q90E81 ID Q90E81 PRELIMINARY; PRT; 164 AA.  
AC Q90E81;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SC29;  
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;  
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from  
RT sichuan."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY037949; AAK72322.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 164  
SQ SEQUENCE 164 AA; 19272 MW; CC3567E17D3D322E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 164;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 52 RVLAVERYLKDQQLGIWGCSGKLC 77

RESULT 299  
Q90E64  
ID Q90E64 PRELIMINARY; PRT; 164 AA.  
AC Q90E64;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SC16;  
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;  
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from  
RT sichuan."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY037966; AAK72339.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 164  
SQ SEQUENCE 164 AA; 19389 MW; 505315DE3C2E2D87 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 164;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 52 RVLAVERYLKDQQLGIWGCSGKLC 77

RESULT 300  
Q90E70  
ID Q90E70 PRELIMINARY; PRT; 164 AA.  
AC Q90E70;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SC20;  
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;  
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from  
RT sichuan."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY037960; AAK72333.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 164  
SQ SEQUENCE 164 AA; 19249 MW; 4218E2E1AF2150EF CRC64;

Query Match 99.3%; Score 138; DB 15; Length 164;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 52 RVLAVERYLKDQQLGIWGCSGKLC 77

RESULT 301  
Q90E82  
ID Q90E82 PRELIMINARY; PRT; 164 AA.  
AC Q90E82;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SC02;  
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;  
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from  
RT sichuan."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY037948; AAK72321.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 164  
SQ SEQUENCE 164 AA; 19246 MW; 0FC57937F2165F31 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 164;  
Best Local Similarity 96.2%; Pred. No. 2.6e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 52 RVLAVERYLKDQQLGIWGCSGKLC 77



RESULT 302  
Q8JER3  
ID Q8JER3 PRELIMINARY; PRT; 180 AA.  
AC Q8JER3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CDNR-1;  
RA Poveda E., Rodes B., Toro C., Martin-Carbonero L., Soriano V.;  
RT "Evolution of the env gene (gp41) in HIV-1 positive patients receiving  
T-20, a fusion inhibitor.";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF500087; AAM21673.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 180 180  
SQ SEQUENCE 180 AA; 21017 MW; 5C1AEE2C3D95AA49 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 180;  
Best Local Similarity 96.2%; Pred. No. 2.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLIC 26  
|:|||||||||||||||||||||  
Db 51 RVLAVERYLKDQQLGIWCGSGKLIC 76  
  
RESULT 303  
Q8JER4  
ID Q8JER4 PRELIMINARY; PRT; 181 AA.  
AC Q8JER4;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CDNR-0;  
RA Poveda E., Rodes B., Toro C., Martin-Carbonero L., Soriano V.;  
RT "Evolution of the env gene (gp41) in HIV-1 positive patients receiving  
T-20, a fusion inhibitor.";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF500086; AAM21672.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 181 181  
SQ SEQUENCE 181 AA; 21126 MW; 27DF2E95E885C2AA CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 181;  
Best Local Similarity 96.2%; Pred. No. 2.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLIC 26  
|:|||||||||||||||||||||

Db 51 RVLAVERYLKDQQLGIWCGSGKLIC 76  
|:|||||||||||||||||||||  
  
RESULT 304  
Q8JAK8  
ID Q8JAK8 PRELIMINARY; PRT; 188 AA.  
AC Q8JAK8;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=96BRRJ101;  
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,  
RA Morgado M.G.;  
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian  
Southeastern and Southern regions.";  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF463436; AAM90812.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR InterPro; IPR00777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1 1  
FT NON\_TER 188 188  
SQ SEQUENCE 188 AA; 21441 MW; 80D9C61680E67E35 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 188;  
Best Local Similarity 96.2%; Pred. No. 3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLIC 26  
|:|||||||||||||||||||||  
Db 87 RVLAVERYLKDQQLGIWCGSGKLIC 112  
  
RESULT 305  
Q8JAJ7  
ID Q8JAJ7 PRELIMINARY; PRT; 190 AA.  
AC Q8JAJ7;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=95BRSP001;  
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,  
RA Morgado M.G.;  
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian  
Southeastern and Southern regions.";  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF463447; AAM90823.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.

DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 190 190  
SQ SEQUENCE 190 AA; 21717 MW; BDA818CAB5A8329F CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 190;  
Best Local Similarity 96.2%; Pred. No. 3.1e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RILAVERYLKDQQLGIWCSGKLIC 26  
|:|||||  
Db 93 RVLAVERYLKDQQLGIWCSGKLIC 118  
|:|||||  
  
RESULT 306  
Q8JAL2 PRELIMINARY; PRT; 192 AA.  
ID Q8JAL2  
AC Q8JAL2;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=95BRRJ019;  
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,  
RA Morgado M.G.;  
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian  
RT Southeastern and Southern regions.";  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF463432; AAM90808.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 192 192  
SQ SEQUENCE 192 AA; 22182 MW; 357E8C354BD97D1A CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 192;  
Best Local Similarity 96.2%; Pred. No. 3.1e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RILAVERYLKDQQLGIWCSGKLIC 26  
|:|||||  
Db 83 RVLAVERYLKDQQLGIWCSGKLIC 108  
|:|||||  
  
RESULT 307  
Q8JAL3 PRELIMINARY; PRT; 199 AA.  
ID Q8JAL3  
AC Q8JAL3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=95BRRJ020;  
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,  
RA Morgado M.G.;  
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian  
RT Southeastern and Southern regions.";  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF463431; AAM90807.1; -.  
DR PIR; A53591; A53591.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 199 199  
SQ SEQUENCE 199 AA; 22918 MW; F6AA8478D3305BC7 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 199;  
Best Local Similarity 96.2%; Pred. No. 3.2e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RILAVERYLKDQQLGIWCSGKLIC 26  
|:|||||  
Db 102 RVLAVERYLKDQQLGIWCSGKLIC 127  
|:|||||

RESULT 308  
Q8JAL5 PRELIMINARY; PRT; 201 AA.  
ID Q8JAL5  
AC Q8JAL5;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=95BRRJ017;  
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,  
RA Morgado M.G.;  
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian  
RT Southeastern and Southern regions.";  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF463429; AAM90805.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 201 201  
SQ SEQUENCE 201 AA; 23181 MW; B3AD0929DEC8020D CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 201;  
Best Local Similarity 96.2%; Pred. No. 3.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RILAVERYLKDQQLGIWCSGKLIC 26  
|:|||||  
Db 92 RVLAVERYLKDQQLGIWCSGKLIC 117  
|:|||||

RESULT 309  
Q8JAL8 ID Q8JAL8 PRELIMINARY; PRT; 201 AA.  
AC Q8JAL8;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=95BRRJ013;  
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,  
RA Morgado M.G.;  
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian  
Southeastern and Southern regions.";  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF463426; AAM90802.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 201 201  
SQ SEQUENCE 201 AA; 23281 MW; 67ABC2E7D2C93E44 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 201;  
Best Local Similarity 96.2%; Pred. No. 3.3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 98 RVLAVERYLKDQQLGIWGCSGKLIC 123  
  
RESULT 310  
Q8JAM0 ID Q8JAM0 PRELIMINARY; PRT; 217 AA.  
AC Q8JAM0;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=95BRRJ011;  
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,  
RA Morgado M.G.;  
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian  
Southeastern and Southern regions.";  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF463424; AAM90800.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 217 217  
SQ SEQUENCE 217 AA; 24952 MW; 3F41BA3210A46167 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 217;  
Best Local Similarity 96.2%; Pred. No. 3.5e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 117 RVLAVERYLKDQQLGIWGCSGKLIC 142  
  
RESULT 311  
Q99IC1 ID Q99IC1 PRELIMINARY; PRT; 225 AA.  
AC Q99IC1;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope polyprotein (Fragment).  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,  
RA Zivny I., Jarry W., Pozzi L., Kurane I., Ennis F.;  
RT "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established  
at two different time points: Role of CTL in the emergence of escaped  
mutants.";  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB047355; BAB32636.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 225 225  
SQ SEQUENCE 225 AA; 25618 MW; B8A1E50F503D2A9A CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 225;  
Best Local Similarity 96.2%; Pred. No. 3.7e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 68 RVLAVERYLKDQQLGIWGCSGKLIC 93  
  
RESULT 312  
Q99IB9 ID Q99IB9 PRELIMINARY; PRT; 225 AA.  
AC Q99IB9;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope polyprotein (Fragment).  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,  
RA Zivny I., Jarry W., Pozzi L., Kurane I., Ennis F.;  
RT "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established  
at two different time points: Role of CTL in the emergence of escaped  
mutants.";  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB047357; BAB32638.1; -.

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DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Polypeptide; Transmembrane.
FT NON_TER 1
FT NON_TER 225
SQ SEQUENCE 225 AA; 25557 MW; C5660AEB589DDFA6 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 225;
Best Local Similarity 96.2%; Pred. No. 3.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db 68 RVLAVERYLKDQQLGIWCSGKLC 93

RESULT 313
Q99IC4
ID Q99IC4 PRELIMINARY; PRT; 225 AA.
AC Q99IC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
RA Zivny I., Jarry W., Pozzi L., Kurane I., Ennis F.;
RT "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
RT at two different time points: Role of CTL in the emergence of escaped
RT mutants.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047352; BAB32633.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Polypeptide; Transmembrane.
FT NON_TER 1
FT NON_TER 225
SQ SEQUENCE 225 AA; 25480 MW; C2166441900478ED CRC64;

Query Match 99.3%; Score 138; DB 15; Length 225;
Best Local Similarity 96.2%; Pred. No. 3.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db 68 RVLAVERYLKDQQLGIWCSGKLC 93

RESULT 314
Q99IC3
ID Q99IC3 PRELIMINARY; PRT; 225 AA.
AC Q99IC3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
RA Zivny I., Jarry W., Pozzi L., Kurane I., Ennis F.;
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RT "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
RT at two different time points: Role of CTL in the emergence of escaped
RT mutants.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047353; BAB32634.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Polypeptide; Transmembrane.
FT NON_TER 1
FT NON_TER 225
SQ SEQUENCE 225 AA; 25609 MW; 6C1A3A0334931031 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 225;
Best Local Similarity 96.2%; Pred. No. 3.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db 68 RVLAVERYLKDQQLGIWCSGKLC 93

RESULT 315
Q99IC5
ID Q99IC5 PRELIMINARY; PRT; 225 AA.
AC Q99IC5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
RA Zivny I., Jarry W., Pozzi L., Kurane I., Ennis F.;
RT "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
RT at two different time points: Role of CTL in the emergence of escaped
RT mutants.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047351; BAB32632.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Polypeptide; Transmembrane.
FT NON_TER 1
FT NON_TER 225
SQ SEQUENCE 225 AA; 25527 MW; EB6B83E37AD63B04 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 225;
Best Local Similarity 96.2%; Pred. No. 3.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db 68 RVLAVERYLKDQQLGIWCSGKLC 93

RESULT 316
Q99IC0
ID Q99IC0 PRELIMINARY; PRT; 225 AA.
AC Q99IC0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
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OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,  
RA Zivny I., Jarry W., Pozzi L., Kurane I., Ennis F.;  
RT "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established  
RT at two different time points: Role of CTL in the emergence of escaped  
RT mutants.";  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB047356; BAB32637.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Polyprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 225  
SQ SEQUENCE 225 AA; 25579 MW; B9013F57411CDDCB CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 225;  
Best Local Similarity 96.2%; Pred. No. 3.7e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 68 RVLAVERYLKDQQLGIWCGSGKLC 93  
  
RESULT 317  
Q78118  
ID Q78118 PRELIMINARY; PRT; 357 AA.  
AC Q78118;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope protein, gp120 /gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92144209; PubMed=1736940;  
RA Steuler H., Storch-Hagenlocher B., Wildemann B.;  
RT "Distinct populations of Human immunodeficiency virus type 1 in blood  
RT and cerebrospinal fluid.";  
RL AIDS Res. Hum. Retroviruses 8:53-59(1992).  
DR EMBL; X61355; CAA43622.1; --  
DR PIR; S21994; S21994.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
SQ SEQUENCE 357 AA; 41140 MW; CE87EB06A73CDCA4 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 357;  
Best Local Similarity 96.2%; Pred. No. 5.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 80 RVLAVERYLKDQQLGIWCGSGKLC 105  
  
RESULT 318  
Q78156  
ID Q78156 PRELIMINARY; PRT; 357 AA.  
AC Q78156;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope protein, gp120 /gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92144209; PubMed=1736940;  
RA Steuler H., Storch-Hagenlocher B., Wildemann B.;  
RT "Distinct populations of Human immunodeficiency virus type 1 in blood  
RT and cerebrospinal fluid.";  
RL AIDS Res. Hum. Retroviruses 8:53-59(1992).  
DR EMBL; X61354; CAA43620.1; --  
DR PIR; A53591; A53591.  
DR PIR; S70420; S22006.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
SQ SEQUENCE 357 AA; 41191 MW; 2DC3AC6A7EC40867 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 357;  
Best Local Similarity 96.2%; Pred. No. 5.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 80 RVLAVERYLKDQQLGIWCGSGKLC 105  
  
RESULT 319  
Q78112  
ID Q78112 PRELIMINARY; PRT; 357 AA.  
AC Q78112;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope protein, gp120/gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92144209; PubMed=1736940;  
RA Steuler H., Storch-Hagenlocher B., Wildemann B.;  
RT "Distinct populations of Human immunodeficiency virus type 1 in blood  
RT and cerebrospinal fluid.";  
RL AIDS Res. Hum. Retroviruses 8:53-59(1992).  
DR EMBL; X61358; CAA43628.1; --  
DR PIR; S70424; S21992.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
SQ SEQUENCE 357 AA; 41248 MW; C3E22F3EF8C4847E CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 357;  
Best Local Similarity 96.2%; Pred. No. 5.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 80 RVLAVERYLKDQQLGIWCGSGKLC 105

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RESULT 320
Q78155
ID Q78155 PRELIMINARY; PRT; 357 AA.
AC Q78155;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein, gp120 /gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92144209; PubMed=1736940;
RA Steuler H., Storch-Hagenlocher B., Wildemann B.;
RT "Distinct populations of Human immunodeficiency virus type 1 in blood
and cerebrospinal fluid.";
RL AIDS Res. Hum. Retroviruses 8:53-59(1992).
DR EMBL; X61353; CAA43618.1; -.
DR PIR; A53591; A53591.
DR PIR; S22004; S22004.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 357 AA; 41152 MW; 07462A9B4505C734 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 357;
Best Local Similarity 96.2%; Pred. No. 5.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 80 RVLAVERYLKDQQLGIWGCSGKLIC 105
|:|||||

RESULT 321
Q9WIT0
ID Q9WIT0 PRELIMINARY; PRT; 362 AA.
AC Q9WIT0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 protein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=97NOGIL3C;
RC MEDLINE=20092438; PubMed=10628816;
RA Jonassen T.O., Grinde B., Asjo B., Hasle G., Hungnes O.;
RT "Inter-subtype recombinant HIV-1 involving HIV-MAL-like and subtype H-
like sequence in four Norwegian cases.";
RL AIDS Res. Hum. Retroviruses 16:49-58(2000).
DR EMBL; AJ237569; CAB39745.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 362 AA; 41388 MW; E5DFF443EC39FFED CRC64;
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Query Match 99.3%; Score 138; DB 15; Length 362;
Best Local Similarity 96.2%; Pred. No. 6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 86 RVLAVERYLKDQQLGIWGCSGKLIC 111
|:|||||

RESULT 322
Q8QDX2
ID Q8QDX2 PRELIMINARY; PRT; 380 AA.
AC Q8QDX2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=98BY10443;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
virus type 1 genomes of prevalent strains among IDUs in countries of
the FSU.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF414005; AAL78485.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 380 AA; 43859 MW; 42B1798C20603F06 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 380;
Best Local Similarity 96.2%; Pred. No. 6.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 103 RVLAVERYLKDQQLGIWGCSGKLIC 128
|:|||||

RESULT 323
Q8QE11
ID Q8QE11 PRELIMINARY; PRT; 387 AA.
AC Q8QE11;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=98UA0116;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
virus type 1 genomes of prevalent strains among IDUs in countries of
the FSU.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413981; AAL78436.1; -.
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RESULT 327
O72603
ID O72603 PRELIMINARY; PRT; 398 AA.
AC O72603;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRRJ014;
RX MEDLINE=20199695; PubMed=10737434;
RA Bongertz V., Bou-Habib D.C., Brigido L.F.M., Caseiro M., Chequer P.J.,
RA Couto-Fernandez J.C., Ferreira P.C., Galvao-Castro B., Greco D.,
RA Guimaraes M.L., Linhares de Carvalho M.I., Morgado M.G.,
RA Oliveira C.A., Osmanov S., Ramos C.A., Rossini M., Sabino E.,
RA Tanuri A., Ueda M.;
RT "HIV-1 diversity in Brazil: genetic, biologic, and immunologic
RT characterization of HIV-1 strains in three potential HIV vaccine
RT evaluation sites. Brazilian Network for HIV Isolation and
RT Characterization."
RL J. Acquir. Immune Defic. Syndr. 23:184-193(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRRJ014;
RX MEDLINE=20199695; PubMed=10737434;
RA Bongertz V., Bou-Habib D.C., Brigido L.F.M., Caseiro M., Chequer P.J.,
RA Couto-Fernandez J.C., Ferreira P.C., Galvao-Castro B., Greco D.,
RA Guimaraes M.L., Linhares de Carvalho M.I., Morgado M.G.,
RA Oliveira C.A., Osmanov S., Ramos C.A., Rossini M., Sabino E.,
RA Tanuri A., Ueda M.;
RT "HIV-1 diversity in Brazil: genetic, biologic, and immunologic
RT characterization of HIV-1 strains in three potential HIV vaccine
RT evaluation sites. Brazilian Network for HIV Isolation and
RT Characterization."
RL J. Acquir. Immune Defic. Syndr. 23:184-193(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRRJ014;
RA Guimaraes M.;
RT "High frequency of HIV-1 recombinant genomes in samples from southeast
RT and south regions of Brazil."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF062424; AAC17163.2; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 398
SQ SEQUENCE 398 AA; 44813 MW; 37C31D2C97168E19 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 398;
Best Local Similarity 96.2%; Pred. No. 6.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 308 RVLAVERYLKDQQLGIWGCSGKLIC 333

RESULT 328
O72602
ID O72602 PRELIMINARY; PRT; 416 AA.
AC O72602;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRRJ014;
RX MEDLINE=20199695; PubMed=10737434;
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RA Bongertz V., Bou-Habib D.C., Brigido L.F.M., Caseiro M., Chequer P.J.,
RA Couto-Fernandez J.C., Ferreira P.C., Galvao-Castro B., Greco D.,
RA Guimaraes M.L., Linhares de Carvalho M.I., Morgado M.G.,
RA Oliveira C.A., Osmanov S., Ramos C.A., Rossini M., Sabino E.,
RA Tanuri A., Ueda M.;
RT "HIV-1 diversity in Brazil: genetic, biologic, and immunologic
RT characterization of HIV-1 strains in three potential HIV vaccine
RT evaluation sites. Brazilian Network for HIV Isolation and
RT Characterization."
RL J. Acquir. Immune Defic. Syndr. 23:184-193(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRRJ014;
RA Guimaraes M.;
RT "High frequency of HIV-1 recombinant genomes in samples from southeast
RT and south regions of Brazil."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF062423; AAC17162.2; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 416
SQ SEQUENCE 416 AA; 47011 MW; 3E6244DFAC4A8703 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 416;
Best Local Similarity 96.2%; Pred. No. 6.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 305 RVLAVERYLKDQQLGIWGCSGKLIC 330

RESULT 329
Q8J513
ID Q8J513 PRELIMINARY; PRT; 416 AA.
AC Q8J513;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRRSP004;
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
RA Morgado M.G.;
RT "High Frequency of Recombinant Genomes in HIV-1 Samples From Brazilian
RT Southeastern and Southern Regions."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY071998; AAL62001.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 416
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SQ SEQUENCE 416 AA; 47011 MW; 3E6244DFAC4A8703 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 416;  
Best Local Similarity 96.2%; Pred. No. 6.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||

Db 305 RVLAVERYLKDQQLGIWGCSGKLIC 330

RESULT 330

Q8J514 PRELIMINARY; PRT; 421 AA.

AC Q8J514;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=96BRRJ101;  
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,  
RA Morgado M.G.;  
RT "High Frequency of Recombinant Genomes in HIV-1 Samples From Brazilian  
RT Southeastern and Southern Regions.";  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY071997; AAL62000.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1 421  
FT NON\_TER 421 421  
SQ SEQUENCE 421 AA; 47597 MW; FE05A7E3071758CB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 421;  
Best Local Similarity 96.2%; Pred. No. 7e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||

Db 310 RVLAVERYLKDQQLGIWGCSGKLIC 335

RESULT 331

O41643 PRELIMINARY; PRT; 546 AA.

AC O41643;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PC12;  
RX MEDLINE=98105804; PubMed=9445059;  
RA Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,  
RA Walker B.D., Neumann A.U., Vermund S.H., Mestecky J., Jackson S.,  
RA Fenamore E., Cao Y., Gao F., Kalams S., Kunstman K.J., McDonald D.,

RA McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.;  
RT "Immunological and virological analyses of persons infected by human  
RT immunodeficiency virus type 1 while participating in trials of  
RT recombinant gp120 subunit vaccines.";  
RL J. Virol. 72:1552-1576(1998).  
DR EMBL; U84885; AAC58931.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 1 546  
FT NON\_TER 546 546  
SQ SEQUENCE 546 AA; 61591 MW; B7273DB04581D451 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 546;  
Best Local Similarity 96.2%; Pred. No. 9.2e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||

Db 448 RVLAVERYLKDQQLGIWGCSGKLIC 473

RESULT 332

Q73363 PRELIMINARY; PRT; 605 AA.

AC Q73363;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TH/93/67;  
RX MEDLINE=96303593; PubMed=8744585;  
RA Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,  
RA Daniels R.S.;  
RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,  
RT D, E, and F obtained from the World Health Organization Network for  
RT HIV Isolation and Characterization.";  
RL AIDS Res. Hum. Retroviruses 12:741-747(1996).  
DR EMBL; U39258; AAB37195.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 605 AA; 67420 MW; B384ACADA15AE6FB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 605;  
Best Local Similarity 96.2%; Pred. No. 1e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||

Db 562 RVLAVERYLKDQQLGIWGCSGKLIC 587

RESULT 333

Q9Q6V8

ID Q9Q6V8 PRELIMINARY; PRT; 606 AA.  
AC Q9Q6V8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Truncated envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1] \_\_\_\_\_  
RP SEQUENCE FROM N.A.  
RC STRAIN=KAL153;  
RX MEDLINE=20386750; PubMed=10933619;  
RA Liitsola K., Holm K., Bobkov A., Pokrovski V., Smolskaja T.,  
RA Leinikki P., Osmanov S., Salminen M., UNAIDS Virus Isolation Network;  
RT "An AB recombinant and its parental HIV type 1 strains in the area of  
RT the former soviet union: low requirements for sequence identity in  
RT recombination.";  
RL AIDS Res. Hum. Retroviruses 16:1047-1053 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KAL153;  
RA Liitsola K.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBBJ databases.  
DR EMBL; AF193276; AAF22321.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
KW Transmembrane.  
SQ SEQUENCE 606 AA; 67781 MW; 218C77457D4DFA8A CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 606;  
Best Local Similarity 96.2%; Pred. No. 1e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 563 RVLAVERYLKDQQLGIWGCSGKLIC 588  
|:|||||  
  
RESULT 334  
Q8Q859 PRELIMINARY; PRT; 616 AA.  
ID Q8Q859;  
AC Q8Q859;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp160.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1] \_\_\_\_\_  
RP SEQUENCE FROM N.A.  
RC STRAIN=KR6035;  
RA Daniels R.S., Patel D., Xiang Z., Zheng N.N., Kang C.;  
RT "Evidence for the spread of immune-escape HIV-1 subtype B in the  
RT Korean population.";  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBBJ databases.  
DR EMBL; AJ417419; CAD10131.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 616 AA; 68756 MW; BE55DAE5BA59BC15 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 616;  
Best Local Similarity 96.2%; Pred. No. 1e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 586 RVLAVERYLKDQQLGIWGCSGKLIC 611  
|:|||||  
  
RESULT 335  
Q9IK02 PRELIMINARY; PRT; 679 AA.  
ID Q9IK02;  
AC Q9IK02;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Truncated envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1] \_\_\_\_\_  
RP SEQUENCE FROM N.A.  
RC STRAIN=546hc-F7;  
RA Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;  
RT "Analysis of human immunodeficiency virus type 1 gp160 sequences from  
RT a patient with HIV dementia: evidence for monocyte trafficking into  
RT brain.";  
RL J. Neurovirol. 0:0-0 (2000).  
DR EMBL; AF217165; AAF75507.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
KW Transmembrane.  
SQ SEQUENCE 679 AA; 76494 MW; 69C6485D07902578 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 679;  
Best Local Similarity 96.2%; Pred. No. 1.2e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 584 RVLAVERYLKDQQLGIWGCSGKLIC 609  
|:|||||  
  
RESULT 336  
Q9IK06 PRELIMINARY; PRT; 684 AA.  
ID Q9IK06;  
AC Q9IK06;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1] \_\_\_\_\_  
RP SEQUENCE FROM N.A.  
RC STRAIN=546hc-B6;  
RA Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;  
RT "Analysis of human immunodeficiency virus type 1 gp160 sequences from

RT a patient with HIV dementia: evidence for monocyte trafficking into  
brain.";  
RL J. Neurovirol. 0:0-0(2000).  
DR EMBL; AF217161; AAF75503.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 684 AA; 77266 MW; F9E6F3CCE4D32E10 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 684;  
Best Local Similarity 96.2%; Pred. No. 1.2e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 584 RVLAVERYLKDQQLGIWGCSGKLIC 609

RESULT 337  
Q8Q856 PRELIMINARY; PRT; 729 AA.  
AC Q8Q856;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp160.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KRA812;  
RA Daniels R.S., Patel D., Xiang Z., Zheng N.N., Kang C.;  
RT "Evidence for the spread of immune-escape HIV-1 subtype B in the  
RT Korean population.";  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ417422; CAD10134.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 729 AA; 81920 MW; 97DA9C4263270381 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 729;  
Best Local Similarity 96.2%; Pred. No. 1.2e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 590 RVLAVERYLKDQQLGIWGCSGKLIC 615

RESULT 338  
Q9IW14 PRELIMINARY; PRT; 797 AA.  
AC Q9IW14;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp160.  
GN ENV.

OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=subtype B;  
RA Daniels R.S., Beddows S., Wilson P., Douglas N.W., Patel D.,  
RA Ives K.J., Easterbrook P., Weber J.N.;  
RT "An association between amino acid substitutions in the 'Silent Face'  
RT of Human immunodeficiency virus type 1 gp120 and resistance to  
RT antibody mediated neutralization.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ271111; CAB86164.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 797 AA; 90755 MW; E08DD15846ED4F7 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 797;  
Best Local Similarity 96.2%; Pred. No. 1.4e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||||||||||||||||||  
Db 581 RVLAVERYLKDQQLGIWGCSGKLIC 606

RESULT 339  
Q03808 PRELIMINARY; PRT; 797 AA.  
ID Q03808  
AC Q03808;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein 120/41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88302422; PubMed=2841608;  
RA Fisher A.G., Ensoli B., Looney D., Rose A., Gallo R.C., Saag M.S.,  
RA Shaw G.M., Hahn B.H., Wong-Staal F.;  
RT "Biologically diverse molecular variants within a single HIV-1  
RT isolate.";  
RL Nature 334:444-447(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91374618; PubMed=1895406;  
RA Daniels R.S., Smith M.H., Fisher A.G.;  
RT "Molecular characterization of biologically diverse envelope variants  
RT of human immunodeficiency virus type 1 derived from an individual.";  
RL J. Virol. 65:5574-5578(1991).  
DR EMBL; M37575; AAB04111.1; --  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
FT NON TER 797  
SQ SEQUENCE 797 AA; 90597 MW; F1BCF5E6FD6EB92A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 797;  
Best Local Similarity 96.2%; Pred. No. 1.4e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 572 RVLAVERYLKDQQLGIWGCSGKLIC 597

RESULT 340  
Q03810  
ID Q03810 PRELIMINARY; PRT; 797 AA.  
AC Q03810;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein 120/41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88302422; PubMed=2841608;  
RA Fisher A.G., Ensoli B., Looney D., Rose A., Gallo R.C., Saag M.S.,  
RA Shaw G.M., Hahn B.H., Wong-Staal F.;  
RT "Biologically diverse molecular variants within a single HIV-1  
RT isolate.";  
RL Nature 334:444-447(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91374618; PubMed=1895406;  
RA Daniels R.S., Smith M.H., Fisher A.G.;  
RT "Molecular characterization of biologically diverse envelope variants  
RT of human immunodeficiency virus type 1 derived from an individual.";  
RL J. Virol. 65:5574-5578(1991).  
DR EMBL; M37576; AAB04112.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
FT NON TER 797 797  
SQ SEQUENCE 797 AA; 90888 MW; 081B8A615568B47B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 797;  
Best Local Similarity 96.2%; Pred. No. 1.4e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 572 RVLAVERYLKDQQLGIWGCSGKLIC 597

RESULT 341  
Q03807  
ID Q03807 PRELIMINARY; PRT; 799 AA.  
AC Q03807;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein 120/41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88302422; PubMed=2841608;  
RA Fisher A.G., Ensoli B., Looney D., Rose A., Gallo R.C., Saag M.S.,  
RA Shaw G.M., Hahn B.H., Wong-Staal F.;  
RT "Biologically diverse molecular variants within a single HIV-1  
RT isolate.";  
RL Nature 334:444-447(1988).  
RN [2]

RP SEQUENCE FROM N.A.  
RX MEDLINE=91374618; PubMed=1895406;  
RA Daniels R.S., Smith M.H., Fisher A.G.;  
RT "Molecular characterization of biologically diverse envelope variants  
RT of human immunodeficiency virus type 1 derived from an individual.";  
RL J. Virol. 65:5574-5578(1991).  
DR EMBL; M37574; AAB04110.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
FT NON TER 799 799  
SQ SEQUENCE 799 AA; 90630 MW; 9BE98E53F795327C CRC64;

Query Match 99.3%; Score 138; DB 15; Length 799;  
Best Local Similarity 96.2%; Pred. No. 1.4e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 574 RVLAVERYLKDQQLGIWGCSGKLIC 599

RESULT 342  
Q03809  
ID Q03809 PRELIMINARY; PRT; 801 AA.  
AC Q03809;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein 120/41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88302422;  
RA Fisher A.G., Ensoli B., Looney D., Rose A., Gallo R.C., Saag M.S.,  
RA Shaw G.M., Hahn B.H., Wong-Staal F.;  
RT "Biologically diverse molecular variants within a single HIV-1  
RT isolate.";  
RL Nature 334:444-447(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91374618; PubMed=1895406;  
RA Daniels R.S., Smith M.H., Fisher A.G.;  
RT "Molecular characterization of biologically diverse envelope variants  
RT of human immunodeficiency virus type 1 derived from an individual.";  
RL J. Virol. 65:5574-5578(1991).  
DR EMBL; M37491; AAB04109.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON TER 801 801  
SQ SEQUENCE 801 AA; 90891 MW; 5BF897B938BC4413 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 801;  
Best Local Similarity 96.2%; Pred. No. 1.4e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 576 RVLAVERYLKDQQLGIWGCSGKLIC 601



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RESULT 343
Q9QP04 ID Q9QP04 PRELIMINARY; PRT; 802 AA.
AC Q9QP04;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope (Gp160) (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MP411;
RX MEDLINE=99294894; PubMed=10364493;
RA Triques K., Bourgeois A., Saragosti S., Vidal N., Mpoudi-Ngole E.,
RA Nzilambi N., Apetrei C., Ekwilanga M., Delaporte E., Peeters M.;
RT "High diversity of HIV-1 subtype F strains in Central Africa.";
RL Virology 259:99-109(1999).
DR EMBL; AJ237804; CAB4055.2; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 802 802
SQ SEQUENCE 802 AA; 90885 MW; DB27A3076DACF194 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 802;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLC 26
|:|||||||||
Db 535 RVLAVERYLKDQQLGIWGCSGKLC 560

RESULT 344
Q76121 ID Q76121 PRELIMINARY; PRT; 807 AA.
AC Q76121;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94103665; PubMed=8277197;
RA Mascola J.J., Louwagie J.J., McCutchan F.E., Fischer C.L.,
RA Hegerich P.A., Wagner K.F., Fowler A.K., McNeil J.G., Burke D.S.;
RT "Two antigenically distinct subtypes of human immunodeficiency virus
RT type 1: viral genotype predicts neutralization serotype.";
RL J. Infect. Dis. 169:48-54(1993).
DR EMBL; L14570; AAA43875.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
```

```
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 807 807
SQ SEQUENCE 807 AA; 91339 MW; EA982966E4C41F70 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 807;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLC 26
|:|||||||||
Db 534 RVLAVERYLKDQQLGIWGCSGKLC 559

RESULT 345
O41530 ID O41530 PRELIMINARY; PRT; 813 AA.
AC O41530;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C06;
RX MEDLINE=98105804; PubMed=9445059;
RA Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,
RA Walker B.D., Neumann A.U., Vermund S.H., Mestecky J., Jackson S.,
RA Fenamore E., Cao Y., Gao F., Kalams S., Kunstman K.J., McDonald D.,
RA McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.;
RT "Immunological and virological analyses of persons infected by human
RT immunodeficiency virus type 1 while participating in trials of
RT recombinant gp120 subunit vaccines.";
RL J. Virol. 72:1552-1576(1998).
DR EMBL; U84794; AAC58818.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 813 AA; 91793 MW; AD69BB84A48FC968 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 813;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLC 26
|:|||||||||
Db 586 RVLAVERYLKDQQLGIWGCSGKLC 611

RESULT 346
Q9QSQ7 ID Q9QSQ7 PRELIMINARY; PRT; 832 AA.
AC Q9QSQ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
```

OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VI850;  
RX MEDLINE=20192166; PubMed=10725202;  
RA Laukkanen T., Carr J.K., Janssens W., Liitsola K., Gotte D.,  
RA McCutchan F.E., Op de Coul E., Cornelissen M., Heyndrickx L.,  
RA van der Groen G., Salminen M.O.;  
RT "Virtually full-length subtype F and F/D recombinant HIV-1 from Africa  
and South America.";  
RL Virology 269:95-104(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VI850;  
RA Carr J.K., Kim B., Sanders-Buell E., Salminen M.O., Alaeus A.,  
RA Albert J.A., Birx D.L., McCutchan F.E.;  
RT "HIV-1 isolate VI850 from Zaire, complete genome.";  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF077336; AAD46094.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 832 AA; 93809 MW; 4CE00FD6D9DE269B CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 832;  
Best Local Similarity 96.2%; Pred. No. 1.4e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db :|||||  
555 RVLAVERYLKDQQLGIWGCSGKLC 580  
  
RESULT 347  
Q76074 ID Q76074 PRELIMINARY; PRT; 835 AA.  
AC Q76074;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BK132;  
RX MEDLINE=93143998; PubMed=1489577;  
RA McCutchan F.E., Hegerich P.A., Brennan T.P., Phanuphak P.,  
RA Singharaj P., Jugsuddee A., Berman P.W., Gray A.M., Fowler A.K.,  
RA Burke D.S.;  
RT "Genetic variants of HIV-1 in Thailand.";  
RL AIDS Res. Hum. Retroviruses 8:1887-1895(1992).  
DR EMBL; L03697; AAA81527.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER 835 835

SQ SEQUENCE 835 AA; 94918 MW; 46E3566D8B0C92D6 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 835;  
Best Local Similarity 96.2%; Pred. No. 1.4e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db :|||||  
560 RVLAVERYLKDQQLGIWGCSGKLC 585  
  
RESULT 348  
Q8JDN0 ID Q8JDN0 PRELIMINARY; PRT; 837 AA.  
AC Q8JDN0;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22032414; PubMed=12036486;  
RA Long E.M., Rainwater S.M., Lavreys L., Mandaliya K., Overbaugh J.;  
RT "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5  
Coreceptor for Entry, Regardless of the Genetic Complexity of the  
Infecting Virus.";  
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).  
DR EMBL; AF407148; AAM66195.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 837 AA; 94842 MW; FOCCC4026DF90107 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 837;  
Best Local Similarity 96.2%; Pred. No. 1.4e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
Db :|||||  
560 RVLAVERYLKDQQLGIWGCSGKLC 585  
  
RESULT 349  
Q8JDM6 ID Q8JDM6 PRELIMINARY; PRT; 837 AA.  
AC Q8JDM6;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22032414; PubMed=12036486;  
RA Long E.M., Rainwater S.M., Lavreys L., Mandaliya K., Overbaugh J.;  
RT "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5  
Coreceptor for Entry, Regardless of the Genetic Complexity of the  
Infecting Virus.";  
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).  
DR EMBL; AF407149; AAM66199.1; -.

DR GO:0016021; C:integral to membrane; IEA.  
DR GO:0019028; C:viral capsid; IEA.  
DR GO:0019031; C:viral envelope; IEA.  
DR GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
SQ SEQUENCE 837 AA; 94748 MW; 60B366124081226F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 837;  
Best Local Similarity 96.2%; Pred. No. 1.4e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||||||||||||||||||  
Db 560 RVLAVERYLKDQQLGIWGCSGKLC 585

RESULT 350  
Q9Q6V0 PRELIMINARY; PRT; 838 AA.  
AC Q9Q6V0;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN {1}  
RP SEQUENCE FROM N.A.  
RC STRAIN=RU98001;  
RX MEDLINE=20386750; PubMed=10933619;  
RA Liitsola K., Holm K., Bobkov A., Pokrovski V., Smolskaja T.,  
RA Leinikki P., Osmanov S., Salminen M., UNAIDS Virus Isolation Network;  
RT "An AB recombinant and its parental HIV type 1 strains in the area of  
RT the former soviet union: low requirements for sequence identity in  
RT recombination."  
RL AIDS Res. Hum. Retroviruses 16:1047-1053(2000).  
RN {2}  
RP SEQUENCE FROM N.A.  
RC STRAIN=RU98001;  
RA Liitsola K.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF193277; AAF22333.1; --  
DR GO:0016021; C:integral to membrane; IEA.  
DR GO:0019028; C:viral capsid; IEA.  
DR GO:0019031; C:viral envelope; IEA.  
DR GO:0005198; F:structural molecule activity; IEA.  
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DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
SQ SEQUENCE 838 AA; 95247 MW; 127128F8F5D1F86B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 838;  
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Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||||||||||||||||||  
Db 561 RVLAVERYLKDQQLGIWGCSGKLC 586

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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 574 RILAVERYLKDQQLGIWGCSGKLC 599

RESULT 2
ENV_HV1MF STANDARD; PRT; 853 AA.
AC P19551;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11704;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317877; PubMed=1695254;
RA Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meier C.,
RA Wasiak A.;
RT "Cloning and characterization of human immunodeficiency virus type 1
RT variants diminished in the ability to induce syncytium-independent
RT cytolysis."
RL J. Virol. 64:3792-3803(1990).
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CC or send an email to license@isb-sib.ch).
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DR HIV; M33943; ENV$MFA.
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FT CHAIN 510 853 TRANSMEMBRANE GLYCOPROTEIN.
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Query Match 100.0%; Score 139; DB 1; Length 853;
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 577 RILAVERYLKDQQLGIWGCSGKLC 602

RESULT 3
ENV_HV1Z2
ID ENV_HV1Z2 STANDARD; PRT; 853 AA.
AC P12487;
DT 01-OCT-1989 (Rel. 12, Created)
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DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane  
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (Z2/CDC-Z34 isolate) (HIV-1).  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11683;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Theodore T., Buckler-White A.;  
RL Submitted (NOV-1988) to the HIV data bank.  
CC -----  
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DR PIR; S54384; S54384.  
DR HIV; M22639; ENV\$Z2Z6.  
DR InterPro; IPR000328; Env GP41.  
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KW Signal.  
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FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.  
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SQ SEQUENCE 853 AA; 97043 MW; 849B0B8CBFAFF7008 CRC64;

Query Match 100.0%; Score 139; DB 1; Length 853;  
Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RILAVERYLKDQQLGIWCGSGKLC 26  
Db 576 RILAVERYLKDQQLGIWCGSGKLC 601  
RESULT 4  
ENV\_HV1Z6  
ID ENV HV1Z6 STANDARD; PRT; 855 AA.  
AC P04580;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane  
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11708;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87248097; PubMed=3036660;  
RA Srinivasan A., Anand R., York D., Ranganathan P., Feorino P.,  
RA Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,  
RA Sanchez-Pescador R.;  
RT "Molecular characterization of human immunodeficiency virus from  
RT Zaire: nucleotide sequence analysis identifies conserved and variable  
RT domains in the envelope gene.";  
RL Gene 52:71-82(1987).  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; K03458; AAA45380.1; -.  
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DR HIV; K03458; ENV\$Z6.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
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DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
KW Signal.  
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QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
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RESULT 5
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AC P03375;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11678;
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RX MEDLINE=85111123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).
RN [2]
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
RT potential glycosylation sites of the type 1 recombinant human
RT immunodeficiency virus envelope glycoprotein (gp120) expressed in
RT Chinese hamster ovary cells.";
RL J. Biol. Chem. 265:10373-10382(1990).
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CC -----
DR EMBL; M15654; AAA44205.1; -.
DR PIR; A03973; VCLJH3.
DR HIV; M15654; ENV$BH102.
DR InterPro; IPR000328; Env GP41.
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DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
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FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .)
SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A18931BB27 CRC64;

Query Match 100.0%; Score 139; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
   |||||
Db 579 RILAVERYLKDQQLGIWGCSGKLIC 604

RESULT 6
ENV HV1H2
ID - ENV HV1H2 STANDARD; PRT; 856 AA.
AC P04578; O09779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
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FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 386 386 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;
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Query Match 100.0%; Score 139; DB 1; Length 856;  
Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 579 RILAVERYLKDQQLGIWGCSGKLIC 604

RESULT 8  
ENV HV1PV  
ID ENV HV1PV STANDARD; PRT; 856 AA.  
AC P03376;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11700;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85111157; PubMed=2982104;  
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,  
RA Capon D.J.;  
RT "Nucleic acid structure and expression of the human  
RT AIDS/lymphadenopathy retrovirus.";  
RL Nature 313:450-458(1985).  
CC -----

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CC -----  
DR EMBL; K02083; AAB59873.1; -.  
DR EMBL; X01762; CAA25903.1; ALT\_SEQ.  
DR PIR; A03974; VCLJVL.  
DR HIV; K02083; ENVSPV22.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
KW Signal.  
FT SIGNAL 1 30  
FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.  
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.  
FT DISULFID 54 74 BY SIMILARITY.  
FT DISULFID 119 205 BY SIMILARITY.  
FT DISULFID 126 196 BY SIMILARITY.  
FT DISULFID 131 157 BY SIMILARITY.  
FT DISULFID 218 247 BY SIMILARITY.  
FT DISULFID 228 239 BY SIMILARITY.  
FT DISULFID 296 331 BY SIMILARITY.  
FT DISULFID 378 445 BY SIMILARITY.  
FT DISULFID 385 418 BY SIMILARITY.  
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).  
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FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).  
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FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).  
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FT CARBOHYD 386 386 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 625 625 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 674 674 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 750 750 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 816 816 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 856 AA; 97339 MW; 5FCDB1DC3C1209B3 CRC64;

Query Match 100.0%; Score 139; DB 1; Length 856;  
Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 579 RILAVERYLKDQQLGIWGCSGKLIC 604

RESULT 9  
ENV HV1B  
ID ENV HV1B STANDARD; PRT; 861 AA.  
AC P03377;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane  
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).  
OC Viruses; Retrovirus; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11686;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85099333; PubMed=2981635;  
RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;  
RT "Nucleotide sequence of the AIDS virus, LAV.";  
RL Cell 40:9-17(1985).  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; K02013; AAB59751.1; --  
DR EMBL; A04321; CAA00352.1; --  
DR PIR; A03975; VCLJLV.  
DR PDB; 1ERF; 20-FEB-02.  
DR HIV; K02013; ENVSRU.  
DR InterPro; IPR000328; Env GP41.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;  
KW 3D-structure.  
FT SIGNAL 1 30  
FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.  
FT CHAIN 517 861 TRANSMEMBRANE GLYCOPROTEIN.  
FT DISULFID 54 74 BY SIMILARITY.  
FT DISULFID 119 210 BY SIMILARITY.  
FT DISULFID 126 201 BY SIMILARITY.  
FT DISULFID 131 162 BY SIMILARITY.  
FT DISULFID 223 252 BY SIMILARITY.  
FT DISULFID 233 244 BY SIMILARITY.  
FT DISULFID 301 336 BY SIMILARITY.  
FT DISULFID 383 450 BY SIMILARITY.  
FT DISULFID 390 423 BY SIMILARITY.  
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FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 630 630 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 642 642 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 679 679 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 755 755 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 821 821 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 861 AA; 97487 MW; 04DE2B4D4E4FD63A CRC64;  
Query Match 100.0%; Score 139; DB 1; Length 861;  
Best Local Similarity 100.0%; Pred. No. 1.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWCGSGKLIC 26  
Db 584 RILAVERYLKDQQLGIWCGSGKLIC 609  
RESULT 10  
ENV\_HV1J3  
ID ENV\_HV1J3 STANDARD; PRT; 867 AA.  
AC P12489;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane  
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).  
OC Viruses; Retrovirus; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11694;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89352108; PubMed=2669897;  
RA Komiya N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;  
RT "Nucleotide sequences of gag and env genes of a Japanese isolate of  
RT HIV-1 and their expression in bacteria.";  
RL AIDS Res. Hum. Retroviruses 5:411-419(1989).  
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CC -----  
DR EMBL; M21138; AAB03526.1; --  
DR HIV; M21138; ENV\$JH3.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
KW Signal.  
FT SIGNAL 1 30  
FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.  
FT CHAIN 517 867 TRANSMEMBRANE GLYCOPROTEIN.  
FT DISULFID 53 73 BY SIMILARITY.  
FT DISULFID 118 217 BY SIMILARITY.  
FT DISULFID 125 208 BY SIMILARITY.  
FT DISULFID 130 160 BY SIMILARITY.  
FT DISULFID 230 259 BY SIMILARITY.  
FT DISULFID 240 251 BY SIMILARITY.  
FT DISULFID 308 342 BY SIMILARITY.  
FT DISULFID 388 457 BY SIMILARITY.  
FT DISULFID 395 430 BY SIMILARITY.  
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 867 AA; 98399 MW; 5F2310146B8E8680 CRC64;  
  
Query Match 100.0%; Score 139; DB 1; Length 867;  
Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 590 RILAVERYLKDQQLGIWGCSGKLC 615  
  
RESULT 11  
ENV\_HV1S1  
ID ENV HV1S1 STANDARD; PRT; 847 AA.  
AC P19550;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane  
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11691;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90347835; PubMed=2384920;  
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;  
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or  
macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";  
RL J. Virol. 64:4390-4398 (1990).  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M65024; AAA45072.1; -.  
DR PDB; 1OBE; 15-MAY-97.  
DR HIV; M38428; ENV\$SF162.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;  
FT 3D-structure. 1 29  
FT SIGNAL 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.  
FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 BY SIMILARITY.  
FT DISULFID 118 203 BY SIMILARITY.  
FT DISULFID 125 194 BY SIMILARITY.  
FT DISULFID 130 155 BY SIMILARITY.  
FT DISULFID 216 245 BY SIMILARITY.  
FT DISULFID 226 237 BY SIMILARITY.  
FT DISULFID 294 328 BY SIMILARITY.  
FT DISULFID 374 435 BY SIMILARITY.  
FT DISULFID 381 408 BY SIMILARITY.  
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 847 AA; 96135 MW; 0A901317FD7FF2AB CRC64;  
  
Query Match 99.3%; Score 138; DB 1; Length 847;  
Best Local Similarity 96.2%; Pred. No. 2e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWGCSGKLC 26  
|:|||||  
Db 570 RILAVERYLKDQQLGIWGCSGKLC 595  
  
RESULT 12  
ENV\_HV1B1  
ID ENV HV1B1 STANDARD; PRT; 852 AA.  
AC P12488;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane  
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11693;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89085613; PubMed=2789516;  
RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.,  
RA Dandekar S.;  
RT "Biological and molecular characterization of human immunodeficiency  
RT virus (HIV-1BR) from the brain of a patient with progressive  
RT dementia.";  
RL Virology 168:79-89 (1989).  
CC -!- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS  
CC HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

22

DR EMBL; M21098; AAA44221.1; -.  
DR PIR; A31667; VCLJBR.  
DR PDB; 1IM7; 23-OCT-02.  
DR HIV; M21098; ENV\$BRVA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;  
KW





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FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 153 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 331 BY SIMILARITY.
FT DISULFID 379 445 BY SIMILARITY.
FT DISULFID 386 418 BY SIMILARITY.
FT CARBOHYD 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 355 355 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 461 461 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 465 465 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96909 MW; 8396E3F8BBD174E CRC64;
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Query Match 98.6%; Score 137; DB 1; Length 856;  
Best Local Similarity 96.2%; Pred. No. 2.9e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLIIC 26  
|:|||||:|||||:|||||:|||||:|  
Db 579 RILAVERYLKDQQLGIWGCSGKIIC 604

RESULT 16  
ENV\_HV1JR  
ID ENV HV1JR STANDARD; PRT; 848 AA.  
AC P20871;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11688;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Koyanagi S., Chen I.S.Y.;  
RL Submitted (DEC-1988) to the HIV data bank.

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CC -----  
DR EMBL; M38429; AAB03749.1; -.  
DR PDB; 1CE4; 18-MAR-99.  
DR HIV; M38429; ENV$JRCSF.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;  
KW 3D-structure.  
FT SIGNAL 1 32  
FT CHAIN 33 503 EXTERIOR MEMBRANE GLYCOPROTEIN.  
FT CHAIN 504 848 TRANSMEMBRANE GLYCOPROTEIN.  
FT DISULFID 53 73 BY SIMILARITY.  
FT DISULFID 118 203 BY SIMILARITY.  
FT DISULFID 125 194 BY SIMILARITY.  
FT DISULFID 130 154 BY SIMILARITY.  
FT DISULFID 216 245 BY SIMILARITY.  
FT DISULFID 226 237 BY SIMILARITY.  
FT DISULFID 294 328 BY SIMILARITY.  
FT DISULFID 374 437 BY SIMILARITY.  
FT DISULFID 381 410 BY SIMILARITY.  
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).  
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FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 228 228 N-LINKED (GLCNAC. .) (POTENTIAL).  
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FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).  
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FT CARBOHYD 299 299 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 329 329 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 382 382 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 388 388 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 403 403 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 440 440 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 453 453 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 603 603 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 617 617 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 629 629 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 808 808 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 848 AA; 96475 MW; 20767F51227EC3F3 CRC64;
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Query Match 97.8%; Score 136; DB 1; Length 848;  
Best Local Similarity 92.3%; Pred. No. 4.1e-13;  
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLIIC 26  
|:|||||:|||||:|||||:|||||:|  
Db 571 RILAVERYLKDQQLGIWGCSGKLIIC 596

RESULT 17  
ENV\_HV1Y2  
ID ENV HV1Y2 STANDARD; PRT; 843 AA.  
AC P35961;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

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OX NCBI_TaxID=36377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93021387; PubMed=1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
RA Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological
RT properties of human immunodeficiency virus type 1 in vivo: evidence
RT for limited defectiveness and complementation.";
RL J. Virol. 66:6587-6600(1992).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M93258; -; NOT_ANNOTATED_CDS.
DR PIR; H44001; H44001.
DR PDB; 1G9N; 27-DEC-00.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 489 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 490 843 TRANSMEMBRANE GLYCOPROTEIN.
FT TRANSMEM 738 755 POTENTIAL.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 201 BY SIMILARITY.
FT DISULFID 125 192 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 214 243 BY SIMILARITY.
FT DISULFID 224 235 BY SIMILARITY.
FT DISULFID 292 326 BY SIMILARITY.
FT DISULFID 373 432 BY SIMILARITY.
FT DISULFID 380 405 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 381 381 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 395 395 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 598 598 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 803 803 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 843 AA; 95648 MW; C69DFD971C918B71 CRC64;
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Query Match 97.1%; Score 135; DB 1; Length 843;  
Best Local Similarity 92.3%; Pred. No. 5.9e-13;

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Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RILAVERYLKDQQLGIWCSGKLIC 26
|:|||||:|||||:|||||
Db 566 RVLAVERYLRDQQLGIWCSGKLIC 591

RESULT 18
ENV_HV1W2
ID ENV_HV1W2 STANDARD; PRT; 847 AA.
AC P05880;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RT at risk for AIDS.";
RL Science 232:1548-1553(1986).
CC -!- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M12507; AAB12990.1; -.
DR HIV; M12507; ENV$WMJ2.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 501 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 502 847 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 202 BY SIMILARITY.
FT DISULFID 125 193 BY SIMILARITY.
FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 215 244 BY SIMILARITY.
FT DISULFID 225 236 BY SIMILARITY.
FT DISULFID 293 326 BY SIMILARITY.
FT DISULFID 372 435 BY SIMILARITY.
FT DISULFID 379 408 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 847 AA; 96466 MW; CD1E33D73AA5BCAE CRC64;

Query Match 97.1%; Score 135; DB 1; Length 847;
Best Local Similarity 92.3%; Pred. No. 5.9e-13;
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 570 RVLAVERYLRDQQLGIWGCSGKLIC 595

RESULT 19
ENV_HV1S3
ID ENV HV1S3 STANDARD; PRT; 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome.";
RL J. Virol. 64:4016-4020(1990).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY352275; AAQ17031.1; -.
DR PDB; 1MEQ; 11-DEC-02.
DR HIV; M38427; ENV$SF33.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 156 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
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FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 331 BY SIMILARITY.
FT DISULFID 377 439 BY SIMILARITY.
FT DISULFID 384 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 852 AA; 96663 MW; EE7BBF8D23C9910D CRC64;

Query Match 97.1%; Score 135; DB 1; Length 852;
Best Local Similarity 92.3%; Pred. No. 6e-13;
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db 575 RVLAVERYLRDQQLGIWGCSGKLIC 600

RESULT 20
ENV_HV1A2
ID ENV HV1A2 STANDARD; PRT; 855 AA.
AC P03378;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85090453; PubMed=2578227;
RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
RA Levy J.A., Dina D., Luciw P.A.;
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
RT (ARV-2).";
RL Science 227:484-492(1985).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;

Query Match. 97.1%; Score 135; DB 1; Length 856;
Best Local Similarity 92.3%; Pred. No. 6e-13;
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||:|||||:|||||:|||||
Db 579 RVLAVERYLRDQQLGIWGCSGKLIC 604

RESULT 22
ENV_HV1W1
ID ENV HV1W1 STANDARD; PRT; 856 AA.
AC P31872;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=31678;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
RT "Identification and characterization of conserved and variable
RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of
RT AIDS.";
RL Cell 45:637-648(1986).
CC -!- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
DR PIR; A24774; VCLJ3W.
DR PDB; 1LB0; 04-DEC-02.
DR PDB; 1LCX; 04-DEC-02.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 205 BY SIMILARITY.
FT DISULFID 125 196 BY SIMILARITY.
FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 444 BY SIMILARITY.
FT DISULFID 383 417 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97526 MW; DB68D1E49C404DE9 CRC64;

Query Match 97.1%; Score 135; DB 1; Length 856;
Best Local Similarity 92.3%; Pred. No. 6e-13;
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||:|||||:|||||:|||||
Db 579 RVLAVERYLRDQQLGIWGCSGKLIC 604

RESULT 23
ENV_HV1RH
ID ENV HV1RH STANDARD; PRT; 865 AA.
AC P04579;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11701;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
RT "Identification and characterization of conserved and variable
RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of
RT AIDS.";
RL Cell 45:637-648(1986).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M17451; AAA45057.1; -.
DR HIV; M17451; ENV$RF.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 519 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 520 865 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 218 BY SIMILARITY.
FT DISULFID 125 209 BY SIMILARITY.
FT DISULFID 130 157 BY SIMILARITY.
FT DISULFID 231 260 BY SIMILARITY.
FT DISULFID 241 252 BY SIMILARITY.
FT DISULFID 309 343 BY SIMILARITY.
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FT DISULFID 389 452 BY SIMILARITY. (POTENTIAL).  
FT DISULFID 396 425 BY SIMILARITY. (POTENTIAL).  
FT CARBOHYD 87 129 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 129 136 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 136 139 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 139 156 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 156 193 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 193 194 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 194 197 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 197 198 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 198 203 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 203 210 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 210 247 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 247 254 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 254 275 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 275 289 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 289 302 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 302 308 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 308 314 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 314 344 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 344 351 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 351 367 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 367 397 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 397 403 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 403 407 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 407 413 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 413 418 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 418 455 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 455 471 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 471 620 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 620 625 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 625 634 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 634 646 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 646 825 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 825 865 AA; 97809 MW; 28828BC2314ADCAC CRC64;  
SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADCAC CRC64;

Query Match 97.1%; Score 135; DB 1; Length 865;  
Best Local Similarity 92.3%; Pred. No. 6.1e-13;  
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSEKGLIC 26  
|.|||||:|||||  
Db 588 RILAVERYLKDQQLGIWGCSEKGLIC 613

RESULT 24  
ENV\_HV1C4 STANDARD; PRT; 868 AA.  
AC P05879;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).  
OC Viruses; Retrovirus; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11687;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87041461; PubMed=3490666;  
RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,  
RA Andersen P.R., Devare S.G.;  
RT "Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus isolate reveal significant divergence in its genomic sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).  
RN [2]  
RP SEQUENCE OF 34-43.  
RX MEDLINE=90253924; PubMed=2187500;  
RA Kalyanaraman V.S., Rodriguez V., Veronese F., Rahman R., Lusso P.,  
RA DeVico A.L., Copeland T., Oroszlan S., Gallo R.C., Sarngadharan M.G.;

RT "Characterization of the secreted, native gp120 and gp160 of the human immunodeficiency virus type 1.";  
RT AIDS Res. Hum. Retroviruses 6:371-380(1990).  
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CC -----  
CC EMBL; M13137; AAA44311.1; -.  
DR PIR; C25523; VCLJH4.  
DR HIV; M13137; ENV\$CDC45.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.  
KW SIGNAL 1 33  
FT CHAIN 34 522 EXTERIOR MEMBRANE GLYCOPROTEIN (GP120).  
FT CHAIN 523 868 TRANSMEMBRANE GLYCOPROTEIN.  
FT DISULFID 55 75 BY SIMILARITY.  
FT DISULFID 120 216 BY SIMILARITY.  
FT DISULFID 127 207 BY SIMILARITY.  
FT DISULFID 132 163 BY SIMILARITY.  
FT DISULFID 229 258 BY SIMILARITY.  
FT DISULFID 239 250 BY SIMILARITY.  
FT DISULFID 307 341 BY SIMILARITY.  
FT DISULFID 387 456 BY SIMILARITY.  
FT DISULFID 394 429 BY SIMILARITY.  
FT CARBOHYD 89 89 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 162 162 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 208 208 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 245 245 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 273 273 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 342 342 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 349 349 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 371 371 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 395 395 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 409 409 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 459 459 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 473 473 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 628 628 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 649 649 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 828 828 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 868 AA; 98698 MW; A11527FC52A6F0C8 CRC64;

Query Match 97.1%; Score 135; DB 1; Length 868;  
Best Local Similarity 96.2%; Pred. No. 6.1e-13;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSEKGLIC 26  
|||||  
Db 591 RILAVERYLKDQQLGIWGCSEKGLIC 616





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FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96721 MW; F9CD864DAA0D07A5 CRC64;

Query Match 95.0%; Score 132; DB 1; Length 853;
Best Local Similarity .96.2%; Pred. No. 1.7e-12;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 576 RILAVERYLKDQQLGIWGCSGKHC 601

RESULT 27
ENV_HV1KB STANDARD; PRT; 861 AA.
AC P31819;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (KB-1 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=36375;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92351552; PubMed=1322587;
RA Shimizu H., Hasebe F., Tsuchie H., Morikawa S., Ushijima H.,
RA Kitamura T.;
RT "Analysis of a human immunodeficiency virus type 1 isolate carrying a
RT truncated transmembrane glycoprotein.";
RL Virology 189:534-546(1992).
CC -!- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR UAG OCCURS BETWEEN
CC THE CODONS FOR 729-ALA AND 730-ARG.
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CC -----
DR EMBL; D12582; BAA02124.1; ALT_SEQ.
DR PIR; A42995; VCLJKB.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 35 POTENTIAL.
FT CHAIN 36 517 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 518 861 TRANSMEMBRANE GLYCOPROTEIN.
FT TRANSMEM 690 711 POTENTIAL.
FT DISULFID 59 79 BY SIMILARITY.
FT DISULFID 124 212 BY SIMILARITY.
FT DISULFID 131 203 BY SIMILARITY.
FT DISULFID 136 160 BY SIMILARITY.
FT DISULFID 225 254 BY SIMILARITY.
FT DISULFID 235 246 BY SIMILARITY.
FT DISULFID 303 337 BY SIMILARITY.
FT DISULFID 383 446 BY SIMILARITY.
FT DISULFID 390 419 BY SIMILARITY.
FT CARBOHYD 93 93 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 345 345 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 367 367 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 414 414 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 449 449 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 617 617 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 631 631 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 643 643 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 821 821 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 861 AA; 98116 MW; 3C06787658F0C9DA CRC64;

Query Match 95.0%; Score 132; DB 1; Length 861;
Best Local Similarity 88.5%; Pred. No. 1.8e-12;
Matches 23; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 585 RILAVERYLKDQQLGIWGCSGKFC 610

RESULT 28
ENV_HVIND STANDARD; PRT; 846 AA.
ID ENV_HVIND
AC P18799;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
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FT CARBOHYD 288      288      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301      301      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307      307      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 343      343      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350      350      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 365      365      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396      396      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402      402      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406      406      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412      412      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 455      455      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 468      468      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 469      469      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 472      472      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 618      618      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623      623      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632      632      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 644      644      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 823      823      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 863 AA; 97743 MW; B729CB5A6FAD1641 CRC64;

Query Match      89.9%; Score 125; DB 1; Length 863;
Best Local Similarity 88.5%; Pred. No. 2.2e-11;
Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLI C 26
|:|||||:|||||:|||||:|||||:|
Db 586 RVLAVESYLKQQLGIWGCSGKHIC 611

RESULT 30
ENV_SIVCZ
ID _ENV_SIVCZ STANDARD; PRT; 854 AA.
AC P17281;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90259077; PubMed=2188136;
RA Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
RT "Genetic organization of a chimpanzee lentivirus related to HIV-1.";
RL Nature 345:356-359(1990).
CC -!- SIMILARITY: STRONG, WITH HIV-1 ENV POLYPROTEIN.
CC -----
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CC -----
DR EMBL; X52154; CAA36407.1; -.
DR PIR; S09990; VCLJSI.
DR HIV; X52154; ENV$CPZ.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 500 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 501 854 TRANSMEMBRANE GLYCOPROTEIN.
FT TRANSMEM 501 517 POTENTIAL.
FT TRANSMEM 675 693 POTENTIAL.
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FT TRANSMEM 805      821      POTENTIAL.
FT CARBOHYD 134      134      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140      140      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143      143      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154      154      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158      158      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186      186      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195      195      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239      239      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260      260      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267      267      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274      274      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299      299      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331      331      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336      336      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351      351      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356      356      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384      384      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392      392      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 426      426      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 432      432      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446      446      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450      450      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601      601      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608      608      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616      616      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628      628      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 854 AA; 95803 MW; 2E249AFAD4F2D9B3 CRC64;

Query Match      88.5%; Score 123; DB 1; Length 854;
Best Local Similarity 76.9%; Pred. No. 4.4e-11;
Matches 20; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLI C 26
|:|||||:|||||:|||||:|||||:|
Db 569 RLLAVERYLQDQQLGIWGCSGKAV C 594

RESULT 31
ENV_HV1MA
ID _ENV_HV1MA STANDARD; PRT; 859 AA.
AC P04583;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11697;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86245056; PubMed=2424612;
RA Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus; nucleotide sequence analysis
of two isolates from African patients.";
RL Cell 46:63-74(1986).
CC -----
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CC -----
DR EMBL; X04415; CAA28016.1; -.
DR EMBL; A07116; CAA00623.1; -.
DR PIR; T01672; T01672.
DR HIV; K03456; ENV$MAL.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
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DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
Signal.  
FT SIGNAL 1 30  
FT CHAIN 31 513 EXTERIOR MEMBRANE GLYCOPROTEIN.  
FT CHAIN 514 859 TRANSMEMBRANE GLYCOPROTEIN.  
FT DISULFID 53 73 BY SIMILARITY.  
FT DISULFID 118 210 BY SIMILARITY.  
FT DISULFID 125 201 BY SIMILARITY.  
FT DISULFID 130 162 BY SIMILARITY.  
FT DISULFID 223 252 BY SIMILARITY.  
FT DISULFID 233 244 BY SIMILARITY.  
FT DISULFID 301 334 BY SIMILARITY.  
FT DISULFID 380 445 BY SIMILARITY.  
FT DISULFID 387 418 BY SIMILARITY.  
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 357 357 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 467 467 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 819 819 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 859 AA; 97109 MW; DBCF9AA52E3ABF29 CRC64;

Query Match 86.3%; Score 120; DB 1; Length 859;  
Best Local Similarity 80.8%; Pred. No. 1.3e-10;  
Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26  
|:|||||:|:|:|:|:|:|:|:|:|  
Db 581 RVLAVERYLQDQRLGLGMWGCSGKHC 606  
|:|||||:|:|:|:|:|:|:|:|:|  
RESULT 32  
ENV\_SIVM2  
ID\_ENV\_SIVM2 STANDARD; PRT; 380 AA.  
AC P08810;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)] (Fragment).  
GN ENV.  
OS Simian immunodeficiency virus (Mm251 isolate) (SIV-MAC).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11734;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88122665; PubMed=2893293;  
RA Kestler H.W., Li Y., Naidu Y.M., Butler C.V., Ochs M.F., Jaenel G.,

RA King N.W., Daniel M.D., Desrosiers R.C.;  
RT "Comparison of simian immunodeficiency virus isolates.";  
RL Nature 331:619-622(1988).  
CC -!- MISCELLANEOUS: THIS IS A MACAQUE ISOLATE.  
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CC -----  
DR EMBL; X06879; -, NOT ANNOTATED\_CDS.  
DR HIV; X06879; ENV\$NM251.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 2.  
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane.  
FT NON\_TER 1 1  
FT CHAIN <1 134 EXTERIOR MEMBRANE GLYCOPROTEIN.  
FT CHAIN 135 >380 TRANSMEMBRANE GLYCOPROTEIN.  
FT SITE 343 343 IN-FRAME TERMINATION CODON.  
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT NON\_TER 380 380  
SQ SEQUENCE 380 AA; 43623 MW; COE123B387BE3AF8 CRC64;  
Query Match 60.4%; Score 84; DB 1; Length 380;  
Best Local Similarity 50.0%; Pred. No. 2.1e-05;  
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWCSGKLC 26  
|:|:|:|:|:|:|:|:|:|  
Db 201 RVTAEIKYLDQQLNAWGCAFRQVC 226  
|:|:|:|:|:|:|:|:|:|  
RESULT 33  
ENV\_HV2S2  
ID\_ENV\_HV2S2 STANDARD; PRT; 712 AA.  
AC P32536;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 2 (isolate ST/24.1C#2) (HIV-2).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=31681;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92260681; PubMed=1583738;  
RA Mulligan M.J., Yamshchikov G.V., Ritter G.D. Jr., Gao F., Jin M.J.,  
RA Nail C.D., Spies C.P., Hahn B.H., Compans R.W.;  
RT "Cytoplasmic domain truncation enhances fusion activity by the  
RT exterior glycoprotein complex of human immunodeficiency virus type 2  
RT in selected cell types.";  
RL J. Virol. 66:3971-3975(1992).  
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Query Match 59.7%; Score 83; DB 1; Length 851; Best Local Similarity 50.0%; Pred. No. 7.1e-05; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;									
Qy	1	RILAVERYLKDQQLGIWCSGKLIIC 26							
Db	569	RVTAIEKYLKDAQQLNSWGCAFRQVC 594							
RESULT 36									
ENV_HV2NZ		STANDARD;	PRT;	856	AA.				
AC	P05883;								
DT	01-NOV-1988	(Rel. 09, Created)							
DT	01-NOV-1988	(Rel. 09, Last sequence update)							
DT	15-JUL-1999	(Rel. 38, Last annotation update)							
DE	Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)]								
GN	ENV.								
OS	Human immunodeficiency virus type 2 (isolate NIH-Z) (HIV-2).								
OC	Viruses; Retrovird viruses; Retroviridae; Lentivirus.								
OX	NCBI_TaxID=11719;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=88320359; PubMed=3261862;								
RA	Zagury J.F., Franchini G., Reitz M.S. Jr., Collalti E., Starcich B.R., Hall L., Fagnoli K., Jagodzinski L.L., Guo H.-G., Laure F., Arya S.K., Josephs S.F., Zagury D., Wong-Staal F., Gallo R.C.; "Genetic variability between isolates of human immunodeficiency virus (HIV) type 2 is comparable to the variability among HIV type 1."; Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).								
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CC	EMBL; J03654; AAB00761.1; -.								
DR	HIV; J03654; ENV\$2NIHZ.								
DR	InterPro; IPR000328; Env GP41.								
DR	InterPro; IPR000777; GP120.								
DR	Pfam; PF00516; GP120; 1.								
DR	Pfam; PF00517; GP41; 1.								
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.								
FT	SIGNAL	1	20						
FT	CHAIN	21	492						
FT	CHAIN	493	856						
FT	CARBOHYD	37	37						
FT	CARBOHYD	70	70						
FT	CARBOHYD	79	79						
FT	CARBOHYD	112	112						
FT	CARBOHYD	116	116						
FT	CARBOHYD	128	128						
FT	CARBOHYD	133	133						
FT	CARBOHYD	142	142						
FT	CARBOHYD	182	182						
FT	CARBOHYD	183	183						
FT	CARBOHYD	196	196						
FT	CARBOHYD	228	228						
FT	CARBOHYD	231	231						
FT	CARBOHYD	238	238						
FT	CARBOHYD	262	262						
FT	CARBOHYD	268	268						
FT	CARBOHYD	279	279						
FT	CARBOHYD	290	290						
FT	CARBOHYD	300	300						
FT	CARBOHYD	355	355						
FT	CARBOHYD	390	390						
FT	CARBOHYD	400	400						
FT	CARBOHYD	400	400						
EXTERIOR MEMBRANE GLYCOPROTEIN.									
TRANSMEMBRANE GLYCOPROTEIN.									
N-LINKED (GLCNAC. . .) (POTENTIAL).									
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N-LINKED (GLCNAC. . .) (POTENTIAL).									

















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RESULT 46
ENV_SIVML
ID ENV_SIVML STANDARD; PRT; 880 AA.
AC P11267;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Coat protein GP32; Putative protein ENV-
DE EXTN].
GN ENV.
OS Simian immunodeficiency virus (K78 isolate) (SIV-MAC).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11736;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87187627; PubMed=3646094;
RA Hirsch V., Riedel N., Mullins J.I.;
RT "The genome organization of STLV-3 is similar to that of the AIDS
RT virus except for a truncated transmembrane protein.";
RL Cell 49:307-319(1987).
CC -!- MISCELLANEOUS: THIS IS A MACAQUE ISOLATE.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; M19499; -; NOT ANNOTATED_CDS.
DR PIR; C26737; VCLJS2.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 22
FT CHAIN 23 527 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 528 735 COAT PROTEIN GP32.
FT CHAIN 736 880 PUTATIVE PROTEIN ENV-EXTN.
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 373 373 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 478 478 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 652 652 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 760 760 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 880 AA; 101245 MW; CDED81F91624828F CRC64;

Query Match 58.3%; Score 81; DB 1; Length 880;
Best Local Similarity 46.2%; Pred. No. 0.00015;
Matches 12; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
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QY 1 RILAVERYLKDQQLGIWGSGLKIC 26
Db 594 KVTATKYLKDKQAQLNAWGCAFRQVC 619

RESULT 47
ENV_SIVA1
ID ENV_SIVA1 STANDARD; PRT; 768 AA.
AC P27757;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Simian immunodeficiency virus (AGM155 isolate) (SIV-AGM).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11727;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90156504; PubMed=2304139;
RA Johnson P.R., Fomsgaard A., Allan J., Gravell M., London W.T.,
RA Olmstead R.A., Hirsch V.M.;
RT "Simian immunodeficiency viruses from African green monkeys display
RT unusual genetic diversity.";
RL J. Virol. 64:1086-1092(1990).
CC -!- MISCELLANEOUS: THE 155 ISOLATE IS FROM A MONKEY IMPORTED FROM
CC KENYA.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M29975; AAA91911.1; -.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 538 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 539 768 TRANSMEMBRANE GLYCOPROTEIN.
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 490 490 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 493 493 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 646 646 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 662 662 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 768 AA; 86859 MW; B50A7F9C9005D8D9 CRC64;

Query Match 57.6%; Score 80; DB 1; Length 768;
Best Local Similarity 50.0%; Pred. No. 0.00019;
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FT	CARBOHYD	119	119	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	144	144	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	152	152	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	194	194	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	206	206	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	238	238	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	241	241	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	272	272	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	278	278	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	289	289	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	300	300	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	310	310	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	365	365	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	371	371	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	398	398	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	410	410	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	460	460	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	465	465	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	610	610	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	619	619	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	635	635	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
SQ	SEQUENCE	860 AA;	98931 MW;	C7D24EE10136FEDC	CRC64;	

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Query Match          54.7%;      Score 76;  DB 1;  Length 860;
Best Local Similarity 46.2%;      Pred. No. 0.00088;
Matches 12;  Conservative 6;  Mismatches 8;  Indels 0;  Gaps 0;

```

**Qy**            1 RILAVERYLKDQQLLGIWGCSGKLC 26  
               | : | : | | | | | | | | : |  
**Dd**            577 RVTAIEKYLKHQAOQLNSWGCAPQVC 602

Search completed: May 3, 2004, 06:25:32  
Job time : 25 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2004, 06:21:53 ; Search time 37 Seconds  
(without alignments)  
67.594 Million cell updates/sec

Title: US-09-733-239-1  
Perfect score: 139  
Sequence: 1 RILAVERYLKDQQLLGWCSGKLIC 26

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 72

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%  
Maximum Match 100%  
Listing first 500 summaries

Database : PIR\_78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	357	2 S21996	envelope protein g
2	139	100.0	358	2 S21998	envelope protein g
3	139	100.0	853	2 S54384	envelope polyprote
4	139	100.0	854	2 S13288	env protein - huma
5	139	100.0	855	1 VCLJZR	env polyprotein pr
6	139	100.0	856	1 VCLJH3	env polyprotein pr
7	139	100.0	856	1 VCLJVL	env polyprotein pr
8	139	100.0	861	1 VCLJLV	env polyprotein pr
9	138	99.3	357	2 S22006	envelope protein g
10	138	99.3	357	2 S21994	envelope protein g
11	138	99.3	357	2 S22004	envelope protein g
12	138	99.3	357	2 S21992	envelope protein g
13	138	99.3	852	1 VCLJBR	env polyprotein -
14	137	98.6	856	1 A44963	env polyprotein pr
15	135	97.1	357	2 S21990	envelope protein g
16	135	97.1	358	2 S22002	envelope protein g
17	135	97.1	358	2 S22000	envelope protein g
18	135	97.1	358	2 S70417	env polyprotein p
19	135	97.1	443	2 C41621	env polyprotein M
20	135	97.1	445	2 A41621	env polyprotein D
21	135	97.1	454	2 B41621	env polyprotein pr
22	135	97.1	843	1 H44001	envelope glycoprot
23	135	97.1	852	2 T12016	env polyprotein pr
24	135	97.1	855	1 VCLJA2	env polyprotein pr
25	135	97.1	856	1 VCLJ3W	env polyprotein pr
26	135	97.1	861	1 VCLJSC	env polyprotein pr
27	135	97.1	868	1 VCLJH4	env polyprotein -
28	134	96.4	859	1 VCLJMN	env polyprotein pr
29	132	95.0	729	1 VCLJKX	env polyprotein pr

30	132	95.0	851	2 S33985	env polyprotein -
31	132	95.0	861	1 VCLJKB	env polyprotein pr
32	131	94.2	847	2 T09448	envelope glycoprot
33	131	94.2	847	2 S13289	env protein - huma
34	125	89.9	846	1 VCLJND	env polyprotein pr
35	123	88.5	854	1 VCLJSI	env polyprotein pr
36	120	86.3	859	2 T01672	envelope polyprote
37	98	70.5	863	2 A53034	gag polyprotein -
38	92	66.2	877	2 S49197	envelope protein p
39	91	65.5	104	2 S52930	GP41 ENV protein -
40	89	64.0	855	2 A45713	Env transmembrane
41	86	61.9	859	1 VCLJST	env polyprotein pr
42	84	60.4	869	2 A47665	env protein gp120(
43	84	60.4	881	2 S03068	env protein - huma
44	83	59.7	151	2 S30458	env protein - huma
45	83	59.7	151	2 S30459	env protein - huma
46	83	59.7	151	2 S30448	env protein - huma
47	83	59.7	151	2 S30453	env protein - huma
48	83	59.7	151	2 S30452	env protein - huma
49	83	59.7	151	2 S30450	env protein - huma
50	83	59.7	151	2 S30451	env protein - huma
51	83	59.7	151	2 S30457	env protein - huma
52	83	59.7	151	2 S30456	env protein - huma
53	83	59.7	151	2 S30455	env protein - huma
54	83	59.7	151	2 S30454	env protein - huma
55	83	59.7	366	2 B41565	env polyprotein -
56	83	59.7	712	1 VCLJSA	env polyprotein pr
57	83	59.7	732	2 S46352	env polyprotein -
58	83	59.7	851	2 S12159	env protein - huma
59	83	59.7	852	1 VCLJGG	env polyprotein pr
60	83	59.7	859	1 VCLJCT	env polyprotein pr
61	83	59.7	859	2 S24571	env protein - huma
62	83	59.7	869	2 S53098	envelope polyprote
63	83	59.7	881	1 VCLJG3	env polyprotein -
64	83	59.7	885	2 S04322	env polyprotein -
65	83	59.7	886	2 T11555	env protein - simi
66	83	59.7	887	2 T11566	envelope glycoprot
67	82	59.0	877	2 C46356	env polyprotein -
68	81	58.3	864	1 VCLJG4	env polyprotein pr
69	81	58.3	880	1 VCLJS2	env polyprotein -
70	80	57.6	889	1 VCLJG5	env polyprotein -
71	79	56.8	786	2 S28084	env polyprotein -
72	79	56.8	858	1 VCLJG2	env polyprotein pr

ALIGNMENTS

RESULT 1

S21996  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S70422; S21996  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70422  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-357 <ST2>  
A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129  
A:Experimental source: patient 27L  
A>Note: submitted to the EMBL Data Library, July 1991  
C:Superfamily: type B retrovirus env polyprotein

Query Match 100.0%; Score 139; DB 2; Length 357;  
Best Local Similarity 100.0%; Pred. No. 2.1e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLIC 26

|||||

Db 80 RILAVERYLKDQQLGIWGCSGKLIC 105

RESULT 2  
S21998  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Variety: isolate 28  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C;Accession: S21998; S70425  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR  
A;Reference number: S21990  
A;Accession: S21998  
A;Molecule type: DNA  
A;Residues: 1-358 <STE1>  
A;Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR  
A;Reference number: S70417; MUID:92144209; PMID:1736940  
A;Accession: S70425  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-222, 'X', 224-358 <STE2>  
A;Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
C;Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 139; DB 2; Length 358;  
Best Local Similarity 100.0%; Pred. No. 2.1e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 81 RILAVERYLKDQQLGIWGCSGKLIC 106

RESULT 3  
S54384  
envelope polyprotein - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999  
C;Accession: S54384  
R;Theodore, T.; Buckler-White, A.J.  
submitted to the EMBL Data Library, July 1989  
A;Reference number: S54377  
A;Accession: S54384  
A;Status: preliminary  
A;Molecule type: genomic RNA  
A;Residues: 1-853 <THE>  
A;Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA45370.1; PID:g329385  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: polyprotein

Query Match 100.0%; Score 139; DB 2; Length 853;  
Best Local Similarity 100.0%; Pred. No. 5.2e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 576 RILAVERYLKDQQLGIWGCSGKLIC 601

RESULT 4  
S13288  
env protein - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C;Accession: S13288  
R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.  
Nature 348, 69-73, 1990  
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A;Reference number: S13288; MUID:91043044; PMID:2172833  
A;Accession: S13288  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-854 <OBR>  
C;Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 139; DB 2; Length 854;  
Best Local Similarity 100.0%; Pred. No. 5.2e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 577 RILAVERYLKDQQLGIWGCSGKLIC 602

RESULT 5  
VCLJZR  
env polyprotein precursor - human immunodeficiency virus Zr-6  
N;Alternate names: coat polyprotein  
C;Species: human immunodeficiency virus Zr-6  
C;Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999  
C;Accession: D26192  
R;Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu  
Gene 52, 71-82, 1987  
A;Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti  
A;Reference number: A26192; MUID:87248097; PMID:3036660  
A;Accession: D26192  
A;Molecule type: DNA  
A;Residues: 1-855 <SRI>  
A;Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; PID:g329403  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-855/Product: env polyprotein #status predicted <MAT>  
F;20-500/Product: exterior membrane glycoprotein #status predicted <EXT>  
F;501-855/Product: transmembrane glycoprotein #status predicted <TMW>  
F;87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match 100.0%; Score 139; DB 1; Length 855;  
Best Local Similarity 100.0%; Pred. No. 5.3e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|||||  
Db 578 RILAVERYLKDQQLGIWGCSGKLIC 603

RESULT 6  
VCLJH3  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)  
N;Alternate names: coat polyprotein  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C;Accession: A03973  
R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora  
nberger, J.A.; Papas, T.S.; Ghayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.  
Nature 313, 277-284, 1985  
A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.  
A;Reference number: A93353; MUID:85111123; PMID:2578615  
A;Accession: A03973  
A;Molecule type: DNA  
A;Residues: 1-856 <RAT>  
A;Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
F;1-30/Domain: signal sequence #status predicted <SIG>  
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>

F;512-856/Product: transmembrane glycoprotein #status predicted <TMM>  
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406  
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 139; DB 1; Length 856;  
Best Local Similarity 100.0%; Pred. No. 5.3e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 579 RILAVERYLKDQQLGIWGCSGKLIC 604

RESULT 7  
VCLJVL  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C>Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03974  
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.  
Nature 313, 450-458, 1985  
A>Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovi  
A:Reference number: A93355; MUID:85111157; PMID:2982104  
A:Accession: A03974  
A:Molecule type: DNA  
A:Residues: 1-856 <MUE>  
A:Cross-references: GB:K02083; NID:G555008; PIDN:AAB59873.1; PID:G328559  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypro  
F;1-30/Domain: signal sequence #status predicted <SIG>  
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F;512-856/Product: transmembrane glycoprotein #status predicted <TMM>  
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406  
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 139; DB 1; Length 856;  
Best Local Similarity 100.0%; Pred. No. 5.3e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 579 RILAVERYLKDQQLGIWGCSGKLIC 604

RESULT 8  
VCLJVL  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C>Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03975  
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.  
Cell 40, 9-17, 1985  
A>Title: Nucleotide sequence of the AIDS virus, LAV..  
A:Reference number: A90866; MUID:85099333; PMID:2981635  
A:Accession: A03975  
A:Molecule type: DNA  
A:Residues: 1-861 <WAI>  
A:Cross-references: GB:K02013; NID:G326417; PIDN:AAB59751.1; PID:G326424  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypro  
F;1-30/Domain: signal sequence #status predicted <SIG>  
F;31-516/Product: exterior membrane glycoprotein #status predicted <EXT>  
F;517-861/Product: transmembrane glycoprotein #status predicted <TMM>  
F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411  
F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 139; DB 1; Length 861;  
Best Local Similarity 100.0%; Pred. No. 5.3e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 584 RILAVERYLKDQQLGIWGCSGKLIC 609

RESULT 9  
S22006  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S70420; S22006  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70420  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-357 <ST2>  
A:Cross-references: EMBL:X61354; NID:G60190; PIDN:CAA43620.1; PID:G60191  
A:Experimental source: patient L  
A>Note: submitted to the EMBL Data Library, July 1991  
C:Superfamily: type E retrovirus env polyprotein

Query Match 99.3%; Score 138; DB 2; Length 357;  
Best Local Similarity 96.2%; Pred. No. 3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 80 RVLAVERYLKDQQLGIWGCSGKLIC 105

RESULT 10  
S21994  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate 27B  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S21994; S70421  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determ  
A:Reference number: S21990  
A:Accession: S21994  
A:Molecule type: DNA  
A:Residues: 1-357 <STE1>  
A:Cross-references: EMBL:X61355; NID:G60179; PIDN:CAA43622.1; PID:G60180  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70421  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>  
A:Cross-references: EMBL:X61355; NID:G60179  
C:Superfamily: type E retrovirus env polyprotein

Query Match 99.3%; Score 138; DB 2; Length 357;  
Best Local Similarity 96.2%; Pred. No. 3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||  
Db 80 RVLAVERYLKDQQLGIWGCSGKLIC 105



RESULT 11  
S22004  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Variety: isolate 4B  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C;Accession: S22004; S70419  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined  
A;Reference number: S21990  
A;Accession: S22004  
A;Molecule type: DNA  
A;Residues: 1-357 <STE1>  
A;Cross-references: EMBL:X61353; NID:g60188; PIDN:CAA43618.1; PID:g60189  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined  
A;Reference number: S70417; MUID:92144209; PMID:1736940  
A;Accession: S70419  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-292, 'X', 294-357 <STE2>  
A;Cross-references: EMBL:X61353; NID:g60188  
C;Superfamily: type E retrovirus env polyprotein

Query Match 99.3%; Score 138; DB 2; Length 357;  
Best Local Similarity 96.2%; Pred. No. 3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIIC 26  
|:|||||  
Db 80 RVLAVERYLKDQQLGIWGCSGKLIIC 105

RESULT 12  
S21992  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C;Accession: S70424; S21992  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined  
A;Reference number: S70417; MUID:92144209; PMID:1736940  
A;Accession: S70424  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-357 <ST2>  
A;Cross-references: EMBL:X61358; NID:g60177; PIDN:CAA43628.1; PID:g60178  
A;Experimental source: patient 22  
A;Note: submitted to the EMBL Data Library, July 1991  
C;Superfamily: type E retrovirus env polyprotein

Query Match 99.3%; Score 138; DB 2; Length 357;  
Best Local Similarity 96.2%; Pred. No. 3e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIIC 26  
|:|||||  
Db 80 RVLAVERYLKDQQLGIWGCSGKLIIC 105

RESULT 13  
VCLJBR  
env polyprotein - human immunodeficiency virus type 1 (isolate BR)  
N;Alternate names: coat polyprotein  
N;Contains: coat protein gp120; coat protein gp41  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 16-Feb-1997  
C;Accession: A31667  
R;Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S

Virology 168, 79-89, 1989  
A;Title: Biological and molecular characterization of human immunodeficiency virus (HIV-1)  
A;Reference number: A94389; MUID:89085613; PMID:2789516  
A;Accession: A31667  
A;Molecule type: DNA  
A;Residues: 1-852 <ANA>  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: capsid protein; coat protein; polyprotein; transmembrane protein  
F;1-516/Product: coat protein gp120 #status predicted <CP1>  
F;517-852/Product: coat protein gp41 #status predicted <CP2>

Query Match 99.3%; Score 138; DB 1; Length 852;  
Best Local Similarity 96.2%; Pred. No. 7.4e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIIC 26  
|:|||||  
Db 575 RVLAVERYLKDQQLGIWGCSGKLIIC 600

RESULT 14  
A44963  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)  
N;Alternate names: coat polyprotein  
N;Contains: coat protein gp120; coat protein gp41  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 28-May-1999  
C;Accession: A44963  
R;Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J.  
AIDS Res. Hum. Retroviruses 5, 121-129, 1989  
A;Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nu  
A;Reference number: A44963; MUID:89228766; PMID:2713163  
A;Accession: A44963  
A;Molecule type: DNA  
A;Residues: 1-856 <SRI>  
A;Cross-references: GB:M15896; NID:g329392; PIDN:AAB53948.1; PID:g329394  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-520/Product: coat protein gp120 #status predicted <CP1>  
F;521-856/Product: coat protein gp41 #status predicted <CP2>  
F;684-705/Domain: transmembrane #status predicted <TMN>  
F;87,132,138,152,156,183,198,242,263,277,294,302,339,393,402,411,448,461,462,465,611

Query Match 98.6%; Score 137; DB 1; Length 856;  
Best Local Similarity 96.2%; Pred. No. 1.1e-12;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIIC 26  
|:|||||  
Db 579 RILAVERYLKDQQLGIWGCSGKIIC 604

RESULT 15  
S21990  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Variety: isolate 20  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C;Accession: S21990; S70423  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
A;Reference number: S21990  
A;Accession: S21990  
A;Molecule type: DNA  
A;Residues: 1-357 <STE1>  
A;Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992



N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C;Accession: A41621  
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A;Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A;Reference number: A41621; MUID:92107924; PMID:1763038  
A;Accession: A41621  
A;Molecule type: DNA  
A;Residues: 1-445 <BUR>  
A;Cross-references: GB:M77228; NID:G328627; PIDN:AAB03790.1; PID:G555013  
A;Note: this virus was isolated from the mother  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
F;1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F;254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F;426-445/Domain: transmembrane #status predicted <TMN>  
F;9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:  
Query Match 97.1%; Score 135; DB 2; Length 445;  
Best Local Similarity 92.3%; Pred. No. 1.1e-12;  
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 321 RVLAVERYLRDQQLGIWGCSGKLIC 346  
RESULT 21  
B41621  
env polyprotein D - human immunodeficiency virus type 1 (fragment)  
N;Alternate names: coat polyprotein  
N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 31-Jan-1997  
C;Accession: B41621  
R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A;Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A;Reference number: A41621; MUID:92107924; PMID:1763038  
A;Accession: B41621  
A;Molecule type: DNA  
A;Residues: 1-454 <BUR>  
A;Cross-references: GB:M77279  
A;Note: this virus was isolated from the daughter  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
F;1-262/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F;263-454/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F;435-454/Domain: transmembrane #status predicted <TMN>  
F;9,23,36,42,48,49,78,85,102,108,132,138,142,195,210,214,362,367,376/Binding site: carbo  
Query Match 97.1%; Score 135; DB 2; Length 454;  
Best Local Similarity 92.3%; Pred. No. 1.1e-12;  
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 330 RVLALERYLKDQQLGIWGCSGKLIC 355  
RESULT 22  
H44001  
env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)  
N;Alternate names: coat polyprotein  
N;Contains: coat protein gp120; coat protein gp41

C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Sep-1994  
C;Accession: H44001  
R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.  
J. Virol. 66, 6587-6600, 1992  
A;Title: Complete nucleotide sequence, genome organization, and biological properties of  
A;Reference number: A44001; MUID:93021387; PMID:1404605  
A;Accession: H44001  
A;Molecule type: DNA  
A;Residues: 1-843 <LIY>  
A;Cross-references: GB:M93258  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;19-35/Region: hydrophobic  
F;30-489/Product: coat protein gp120 #status predicted <GP1>  
F;490-843/Product: coat protein gp41 #status predicted <GP2>  
F;499-515/Region: hydrophobic  
F;673-689/Region: hydrophobic  
F;738-755/Domain: transmembrane #status predicted <TMN>  
F;87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435  
Query Match 97.1%; Score 135; DB 1; Length 843;  
Best Local Similarity 92.3%; Pred. No. 2.1e-12;  
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 566 RVLAVERYLRDQQLGIWGCSGKLIC 591  
RESULT 23  
T12016  
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C;Accession: T12016  
R;McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.  
AIDS Res. Hum. Retroviruses 14, 329-337, 1998  
A;Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S  
A;Reference number: Z17379; MUID:98178716; PMID:9519894  
A;Accession: T12016  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-852 <MCC>  
A;Cross-references: EMBL:U90934; NID:G2351783; PIDN:AAC59271.1; PID:G2351784  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
Query Match 97.1%; Score 135; DB 2; Length 852;  
Best Local Similarity 92.3%; Pred. No. 2.1e-12;  
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
Db 575 RVLAVERYLRDQQLGIWGCSGKLIC 600  
RESULT 24  
VCLJJA2  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)  
N;Alternate names: coat polyprotein  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C;Accession: A03976  
R;Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-S  
Science 227, 484-492, 1985  
A;Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).

A;Reference number: A04003; MUID:85090453; PMID:2578227  
A;Accession: A03976  
A;Molecule type: DNA  
A;Residues: 1-855 <SAN>  
A;Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;31-509/Product: exterior membrane glycoprotein #status predicted <EXT>  
F;510-855/Product: transmembrane glycoprotein #status predicted <TMM>  
F;87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458  
F;610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.1%; Score 135; DB 1; Length 855;  
Best Local Similarity 92.3%; Pred. No. 2.1e-12;  
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||:|||||  
Db 578 RVLAVERYLRDQQLGIWGCSGKLIC 603

RESULT 25  
VCLJ3W  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
N;Contains: coat protein gp120; coat protein gp41  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997  
C;Accession: A24774  
R;Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
Cell 45, 637-648, 1986  
A;Title: Identification and characterization of conserved and variable regions in the en  
A;Reference number: A24774; MUID:86218077; PMID:2423250  
A;Accession: A24774  
A;Molecule type: DNA  
A;Residues: 1-856 <STA>  
A;Cross-references: GB:K03455; GB:M38432; NID:g1906382  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-501/Product: coat protein gp120 #status predicted <GP1>  
F;502-847/Product: coat protein gp41 #status predicted <GP2>  
F;87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 97.1%; Score 135; DB 1; Length 856;  
Best Local Similarity 92.3%; Pred. No. 2.2e-12;  
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||:|||||  
Db 579 RVLAVERYLRDQQLGIWGCSGKLIC 604

RESULT 26  
VCLJ3C  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
N;Alternate names: coat polyprotein  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C;Accession: B28922  
R;Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
Virology 164, 531-536, 1988  
A;Title: Envelope sequences of two new United States HIV-1 isolates.  
A;Reference number: A28922; MUID:88219542; PMID:3369091  
A;Accession: B28922  
A;Molecule type: DNA  
A;Residues: 1-861 <GUR>  
C;Genetics:

A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prot  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-861/Product: env polyprotein #status predicted <EPP>  
F;87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,39

Query Match 97.1%; Score 135; DB 1; Length 861;  
Best Local Similarity 92.3%; Pred. No. 2.2e-12;  
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||:|||||  
Db 584 RVLAVERYLRDQQLGIWGCSGKLIC 609

RESULT 27  
VCLJH4  
env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)  
N;Alternate names: coat polyprotein  
N;Contains: coat protein gp120; coat protein gp41  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 16-Jul-1999  
C;Accession: C25523  
R;Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare,  
Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986  
A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human  
A;Reference number: A94136; MUID:87041461; PMID:3490666  
A;Accession: C25523  
A;Molecule type: DNA  
A;Residues: 1-868 <DES>  
A;Cross-references: GB:M13137; NID:g326460; PIDN:AAA44311.1; PID:g326467  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prot  
F;1-521/Product: coat protein gp120 #status predicted <GP1>  
F;522-868/Product: coat protein gp41 #status predicted <GP2>  
F;89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,45

Query Match 97.1%; Score 135; DB 1; Length 868;  
Best Local Similarity 96.2%; Pred. No. 2.2e-12;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26  
|:|||||:|||||  
Db 591 RILAVERYLKDQQLGFWGCSGKLIC 616

RESULT 28  
VCLJMN  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate MN)  
N;Alternate names: coat polyprotein  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C;Accession: A28922  
R;Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-St  
Virology 164, 531-536, 1988  
A;Title: Envelope sequences of two new United States HIV-1 isolates.  
A;Reference number: A28922; MUID:88219542; PMID:3369091  
A;Accession: A28922  
A;Molecule type: DNA  
A;Residues: 1-859 <GUR>  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prot  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-859/Product: env polyprotein #status predicted <EPP>  
F;87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401

Query Match 96.4%; Score 134; DB 1; Length 859;



Best Local Similarity 92.3%; Pred. No. 3.1e-12;  
Matches 24; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLLGIWGCSGKLLIC 26  
|:|||||  
Db 583 RVLAVERYLKDQQLLGFWGCSGKLLIC 608

RESULT 29  
VCLJKB  
env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)  
N;Alternate names: coat polyprotein  
N;Contains: coat protein gp120; coat protein gp32  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 01-Mar-1996  
C;Accession: B42995  
R;Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.  
Virology 189, 534-546, 1992  
A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated  
A;Reference number: A42995; MUID:92351552; PMID:1322587  
A;Accession: B42995  
A;Residues: 1-729 <SHI>  
A;Cross-references: GB:S41266; GB:D01206  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F;1-689/Domain: extracellular #status predicted <EXT>  
F;1-33/Domain: signal sequence #status predicted <SIG>  
F;17-33/Region: hydrophobic #status predicted  
F;34-517/Product: coat protein gp120 #status predicted <CP1>  
F;514-517/Region: cleavage processing #status predicted  
F;518-729/Product: coat protein gp32 #status predicted  
F;518-534/Region: hydrophobic #status predicted  
F;690-711/Domain: transmembrane #status predicted <TM1>  
F;712-729/Domain: intracellular #status predicted <INT>  
F;93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 95.0%; Score 132; DB 1; Length 729;  
Best Local Similarity 88.5%; Pred. No. 5.2e-12;  
Matches 23; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLLGIWGCSGKLLIC 26  
|:|||||  
Db 585 RVLAVERYLKDQQLMGIWGCSGKFLIC 610

RESULT 30  
S33985  
env polyprotein - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C;Accession: S33985  
R;Carlini, F.  
submitted to the EMBL Data Library, November 1991  
A;Reference number: S33979  
A;Accession: S33985  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-851 <CAR>  
A;Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199  
C;Superfamily: type E retrovirus env polyprotein

Query Match 95.0%; Score 132; DB 2; Length 851;  
Best Local Similarity 96.2%; Pred. No. 6.2e-12;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLLGIWGCSGKLLIC 26  
|:|||||  
Db 574 RILAVERYLKDQQLLGIWGCSGKFLIC 599

RESULT 31  
VCLJKB  
env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)  
N;Alternate names: coat polyprotein  
N;Contains: coat protein gp120; coat protein gp41  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 01-Mar-1996  
C;Accession: A42995  
R;Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.  
Virology 189, 534-546, 1992  
A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated  
A;Reference number: A42995; MUID:92351552; PMID:1322587  
A;Accession: A42995  
A;Molecule type: mRNA  
A;Residues: 1-861 <SHI>  
A;Cross-references: GB:S41266; GB:D01206  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F;1-689/Domain: extracellular #status predicted <EXT>  
F;1-33/Domain: signal sequence #status predicted <SIG>  
F;17-33/Region: hydrophobic #status predicted  
F;34-517/Product: coat protein gp120 #status predicted <CP1>  
F;514-517/Region: cleavage processing #status predicted  
F;518-861/Product: coat protein gp41 #status predicted <CP2>  
F;518-534/Region: hydrophobic #status predicted  
F;690-711/Domain: transmembrane #status predicted <TM1>  
F;712-861/Domain: intracellular #status predicted <INT>  
F;756-772/Region: hydrophobic #status predicted  
F;93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 95.0%; Score 132; DB 1; Length 861;  
Best Local Similarity 88.5%; Pred. No. 6.2e-12;  
Matches 23; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLLGIWGCSGKLLIC 26  
|:|||||  
Db 585 RVLAVERYLKDQQLMGIWGCSGKFLIC 610

RESULT 32  
T09448  
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999  
C;Accession: T09448  
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,  
submitted to the EMBL Data Library, July 1996  
A;Reference number: Z16673  
A;Accession: T09448  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 1-847 <PAN>  
A;Cross-references: EMBL:U63632; NID:g1465777; PID:g1465781  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein

Query Match 94.2%; Score 131; DB 2; Length 847;  
Best Local Similarity 92.3%; Pred. No. 8.7e-12;  
Matches 24; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLLGIWGCSGKLLIC 26  
|:|||||  
Db 570 RVLAVERYLGDQQLLGIWGCSGKLLIC 595

RESULT 33  
S13289  
env protein - human immunodeficiency virus type 1

A:Accession: S09990  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-854 <HUE>  
A:Cross-references: EMBL:X52154; NID:G58866; PIDN:CAA36407.1; PID:G58874  
C:Genetics:  
A:Gene: env

C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-500/Product: coat protein gp120 #status predicted <CP1>  
F:501-854/Product: coat protein gp41 #status predicted <CP2>

Accession	Domain	transmembrane	#status	predicted
F:675-693	Domain	transmembrane	#status	predicted <TM2>
F:805-821	Domain	transmembrane	#status	predicted <TM3>
F:134,140,143,154,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,4				

Query Match 88.5%; Score 123; DB 1; Length 854;  
Best Local Similarity 76.9%; Pred. No. 1.5e-10;  
Matches 20; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

DB 569 RLLAVERYLQDQQILGLWGCSGKAVC 594

RESULT 36  
T01672

envelope polyprotein precursor - human immunodeficiency virus type 1  
C.Species: human immunodeficiency virus type 1, HIV-1  
C.Date: 19-Feb-1999 #sequence revision 19-Feb-1999 #text change 21-Jul-2000

C:Accession: T01672  
R:Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.  
Cell 46, 63-74, 1986  
A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two iso-  
A:Reference number: Z14389; MUID:86245056; PMID:2424612  
A:Accession: T01672  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-859 <ALI>  
A:Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28016.1; PID:g60234  
C:Superfamily: type E retrovirus env polyprotein

```
Query Match      86.3%; Score 120; DB 2; Length 859;
Best Local Similarity 80.8%; Pred. No. 4.3e-10;
Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 RILAVERYLKDQLLGIWGCSGKLIC 26  
| : | | | | | | | : | | | | | | |  
Db 581 RVLAVERYLODORLLGMWGCSGRHIC 606

RESULT 37  
A53034

[illegible]

A:Title: Genomic cloning and complete sequence analysis of a highly divergent African h  
A:Reference number: A53034; MUID:94149849; PMID:8107220  
A:Accession: A53034  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-863 <VAN>  
A:Cross-references: GB:L02587  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: polyprotein  
  
Query Match 70.5%; Score 98; DB 2; Length 863;  
Best Local Similarity 61.5%; Pred. No. 1e-06;  
Matches 16; Conservative 6; Mismatches 4; Indels 0; Gaps 0;









**Qy**            1 RILAVERYLKDQLLGIWCSGKLIC 26  
               | : | : | : | : | : | : | : |  
**Db**            23 RVTAIEKYLKDOAKLSNWSGCAFCOV 48

RESULT 52  
S30456  
env protein - human immunodeficiency virus type 2 (fragment)  
C:Species: human immunodeficiency virus type 2, HIV-2  
C:Date: 02-Dec-1993 #sequence\_revision 30-Jan-1998 #text\_change 17-Mar-1999  
C:Accession: S30456  
R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;  
Nature 358, 495-499, 1992  
A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.  
A:Reference number: S30448; MUID:92350299; PMID:1641038  
A:Accession: S30456  
A:Status: translation not shown  
A:Molecule type: nucleic acid  
A:Residues: 1-151 <GAO>  
A:Cross-references: EMBL:M87129  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: coat protein; glycoprotein

```
Query Match          59.7%;      Score 83;  DB 2;  Length 151;
Best Local Similarity 50.0%;      Pred. No. 3.2e-05;
Matches 13;  Conservative 6;  Mismatches 7;  Indels 0;  Gaps 0;
```

**Qy**            1 RILAVERYLKQQLLGIWCSGKLIC 26  
               | : : : : | | | : : |  
**D**b****            23 RVTAIEKYLKDOAKLNSWGCAFRVC 48

RESULT 53  
S30455  
env protein - human immunodeficiency virus type 2 (fragment)  
C;Species: human immunodeficiency virus type 2, HIV-2  
C;Date: 02-Dec-1993 #sequence revision 30-Jan-1998 #text\_change 23-Mar-2001  
C;Accession: S30455; S30461; S30469  
R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;  
Nature 358, 495-499, 1992  
A;Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.  
A;Reference number: S30448; MUID:92350299; PMID:1641038  
A;Accession: S30455  
A;Status: translation not shown  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GAO>  
A;Cross-references: EMBL:M87123  
R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;  
submitted to the EMBL Data Library, December 1992  
A;Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa  
A;Reference number: S30460  
A;Accession: S30461  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GA2>  
A;Cross-references: EMBL:M87131  
A;Accession: S30469  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GA3>  
A;Cross-references: EMBL:M87122  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: coat protein; glycoprotein

Query Match 59.7%; Score 83; DB 2; Length 151;  
Best Local Similarity 50.0%; Pred. No. 3.2e-05;  
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLIC 26

23 RVTAEKYLKDOAKLNSWGCAFCVOC 48

RESULT 54

S30454

env protein - human immunodeficiency  
C;Species: human immunodeficiency vir  
C;Date: 09-May-1997 #sequence revisio  
C;Accession: S30465; S30460; S30462;  
R;Gao, F.; Yue, L.; White, A.T.; Papp  
submitted to the EMBL Data Library, D  
A;Description: Human infection by gen  
A;Reference number: S30460  
A;Accession: S30465  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GAW>  
A;Cross-references: EMBL:M87128  
A;Accession: S30460  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GAW>  
A;Cross-references: EMBL:M87120  
A;Experimental source: clone 22ENVB15  
A;Accession: S30462  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GAF>  
A;Cross-references: EMBL:M87132  
A;Experimental source: clone 22ENVB4  
A;Accession: S30463  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GAA>  
A;Cross-references: EMBL:M87126  
A;Experimental source: clone 22ENVBB3  
A;Accession: S30464  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GAZ>  
A;Cross-references: EMBL:M87127  
A;Experimental source: clone 22ENVBB4  
A;Accession: S30466  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GAY>  
A;Cross-references: EMBL:M87121  
A;Experimental source: clone 22ENVB17  
A;Accession: S30467  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GAH>  
A;Cross-references: EMBL:M87119  
A;Experimental source: clone 22ENVB11  
A;Accession: S30468  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GAS>  
A;Cross-references: EMBL:M87133  
A;Experimental source: clone 22ENVB5  
A;Accession: S30470  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GAN>  
A;Cross-references: EMBL:M87134  
A;Experimental source: clone 22ENVB8  
A;Accession: S30471  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GAG>  
A;Cross-references: EMBL:M87124  
A;Experimental source: clone 22ENVBB1  
A;Accession: S30472  
A;Molecule type: nucleic acid  
A;Residues: 1-151 <GAC>  
A;Cross-references: EMBL:M87125  
A;Experimental source: clone 22ENVBB2  
R;Gao, F.; Yue, L.; White, A.T.; Papp  
Nature 358, 495-499, 1992  
A;Title: Human infection by genetical  
A;Reference number: S30448; MUID:9235  
A;Accession: S30448

A:Accession: S30454  
A:Molecule type: nucleic acid  
A:Residues: 1-151 <GA2>  
A:Cross-references: EMBL:M87118  
C:Superfamily: type E retrovirus

Query Match 59.7%; Score 83; DB 2; Length 151;  
Best Local Similarity 50.0%; Pred. No. 3.2e-05;  
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy	:   :   :   :   :   :   :   :   :	1 RILAVERYLKDQQLGIWGCSGKLIC 26
Db	:   :   :   :   :   :   :   :   :	23 RVTAIEKYLKDOAKLNSWGCAFRVC 48

RESULT 55  
B41565  
env polyprotein - simian immunodeficiency virus (strain stm) (fragment)  
N:Alternate names: coat polyprotein  
N:Contains: amino end of coat protein gp32; carboxyl end of coat protein gp120  
C:Species: simian immunodeficiency virus, SIV  
A:Note: host Macaca arctoides (stump-tailed macaque)  
C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 26-Aug-1999  
C:Accession: B41565  
R:Khan, A.S.; Galvin, T.A.; Lowenstine, L.J.; Jennings, M.B.; Gardner, M.B.; Buckler, C.  
J. Virol. 65, 7061-7065, 1991  
A:Title: A highly divergent simian immunodeficiency virus (SIVstm) recovered from stored  
A:Reference number: A41565; MUID:92046379; PMID:1942258

A:Accession: E110  
A:Molecule type: DNA  
A:Residues: 1-366 <KHA>  
A:Cross-references: GB:X60668; NID:G60525; PIDN:CAA43085.1; PID:G60526  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
F:1-139/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F:140-366/Product: coat protein gp32 (fragment) #status predicted <GP2>  
F:141-157/Domain: transmembrane #status predicted <TM1>  
F:309-325/Domain: transmembrane #status predicted <TM2>  
F:23,75,91,94,239,248,264/Binding site: carbohydrate (Asn) (covalent) #status predicted

Qy	1	RILAVERYLKDQQLGIWGC	26
		:   :   :   :	
Db	206	RVTAIEKYLKDOAQLNSW	231
		:   :   :   :	

RESULT 56  
VCLJS4  
env polyprotein precursor - human immunodeficiency virus type 2 (isolate ST/24.1C/2)  
N:Alternate names: coat polyprotein  
N1:Contains: surface glycoprotein gp120; transmembrane glycoprotein gp41  
C:Species: human immunodeficiency virus type 2, HIV-2  
A>Note: host Homo sapiens (man)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Jul-1999  
C:Accession: A42535  
R:Mulligan, M.J.; Yamshchikov, G.V.; Ritter Jr., G.D.; Gao, F.; Jin, M.J.; Nail, C.D.; S  
J. Virol. 66, 3971-3975, 1992  
A:Title: Cytoplasmic domain truncation enhances fusion activity by the exterior glycopro  
A:Reference number: A42535; MUID:92260681; PMID:1583738

F;20-712/Product: env polypeptide #status predicted <ENV>  
 F;20-501/Product: surface glycoprotein gp120 #status predicted <SGG>  
 F;506-712/Product: transmembrane glycoprotein gp41 #status predicted <TPG>  
 F;507-523/Region: hydrophobic  
 F;675-694/Domain: transmembrane #status predicted <TMN>  
 F;366-69,78,131,119,131,137,145,160,173,200,232,235,242,266,272,283,294,304

Query Match 59.7%; Score 83; DB 1; Length 712;  
Best Local Similarity 50.0%; Pred. No. 0.00016;  
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY	1	RILAVERYLKDQQLLGWCGSKLIC	26
		:   :   :   :	
Db	572	RVTAIEKYLKDDAQLNSWGCAFRQVC	597

RESULT 57  
S46352  
env polyprotein - simian immunodeficiency virus SIVagm (isolate SAB-1)  
C;Species: simian immunodeficiency virus SIVagm  
A;Variety: isolate SAB-1  
C;Date: 25-Dec-1994 #sequence\_revision 14-Feb-1997 #text\_change 20-Sep-1999  
C;Accession: S46352  
R;Jin, M.J.; Hui, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V.M.  
EMBO J. 13, 2935-2947, 1994  
A;Title: Mosaic genome structure of simian immunodeficiency virus from West African g  
A;Reference number: S46335; MUID:94298785; PMID:8026477

Accession: 58551  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-732 <JIN>  
A;Cross-references: EMBL:U04005; NID:G466229; PIDN:AAA21510.1; PID:G466236  
A;Experimental source: isolate SAB-1; sabaesus monkey  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: capsid protein; coat protein; polyprotein

Query Match	59.7%;	Score 83;	DB 2;	Length 732;
Best Local Similarity	50.0%;	Pred. No. 0.00017;		
Matches 13;	Conservative	7;	Mismatches 6;	Indels 0;
				Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLIC 26  
| : | : | : | : | : | : | : | :  
DB 594 RVTALEKYLEDARLNIWGCAFRQVC 619

RESULT 58  
S12159  
env protein - human immunodeficiency virus type 2  
C:Species: human immunodeficiency virus type 2, HIV-2  
C:Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 26-Aug-1999  
C:Accession: S12159  
R:Kuehnelt, H.; Kreutz, R.; Ruebsamen-Waigmann, H.  
Nucleic Acids Res. 18, 6142, 1990  
A:Title: Nucleotide sequence of HIV-2(D194), an isolate from a Gambian case  
A:Reference number: S12152; MUID:91045094; PMID:2235509  
A:Accession: S12159  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

Query Match 59.7%; Score 83; DB 2; Length 851;  
Best Local Similarity 50.0%; Pred. No. 0.00019;  
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26





Matches	13;	Conservative	6;	Mismatches	7;	Indels	0;	Gaps	0;
QY	1	RILAVERYLKDQQLLGIWGCSGKLIC	26						
		:  : : : :	:  :  :						
Db	595	RVSAIEKYLKDQAQLNAWGCAFRQVC	620						
RESULT 64									
S04322									
env polyprotein - simian immunodeficiency virus (mangabey isolate F236)									
N;Contains: 120K glycoprotein; 40K glycoprotein									
C;Species: simian immunodeficiency virus, SIV									
A;Note: host Cercocebus torquatus atys (sooty mangabey)									
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999									
C;Accession: S04322									
R;Hirsch, V.M.; Olmsted, R.A.; Murphey-Corb, M.; Purcell, R.H.; Johnson, P.R.									
Nature 339, 389-392, 1989									
A;Title: An African primate lentivirus (SIV(sm)) closely related to HIV-2.									
A;Reference number: S04237; MUID:89262053; PMID:2786147									
A;Accession: S04322									
A;Status: nucleic acid sequence not shown									
A;Molecule type: genomic RNA									
A;Residues: 1-885 <HIR>									
A;Cross-references: EMBL:X14307; NID:g61741; PIDN:CAA32487.1; PID:g61746									
C;Genetics:									
A;Gene: env									
C;Superfamily: type E retrovirus env polyprotein									
C;Keywords: glycoprotein; polyprotein									
Query Match 59.7%; Score 83; DB 2; Length 885;									
Best Local Similarity 50.0%; Pred. No. 0.0002;									
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;									
QY	1	RILAVERYLKDQQLLGIWGCSGKLIC	26						
		:  : : : :	:  :  :						
Db	598	RVTAIEKYLKDQAQLNSWGCAFRQVC	623						
RESULT 65									
T11555									
env protein - simian immunodeficiency virus SIVsm									
C;Species: simian immunodeficiency virus SIVsm									
A;Variety: strain 62									
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000									
C;Accession: T11555									
R;Hirsch, V.M.; Martin, J.E.; Dapolito, G.; Elkins, W.R.; London, W.T.; Goldstein, S.; J									
J. Virol. 68, 2649-2661, 1994									
A;Title: Spontaneous substitutions in the vicinity of the V3 analog affect cell tropism									
A;Reference number: Z17284; MUID:94187106; PMID:8139042									
A;Accession: T11555									
A;Status: preliminary; translated from GB/EMBL/DBJ									
A;Molecule type: DNA									
A;Residues: 1-886 <HIR>									
A;Cross-references: EMBL:U04985; NID:g451609; PIDN:AAA18063.1; PID:g451611									
C;Genetics:									
A;Gene: env									
C;Superfamily: type E retrovirus env polyprotein									
Query Match 59.7%; Score 83; DB 2; Length 886;									
Best Local Similarity 50.0%; Pred. No. 0.0002;									
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;									
QY	1	RILAVERYLKDQQLLGIWGCSGKLIC	26						
		:  : : : :	:  :  :						
Db	599	RVTAIEKYLKDQAQLNSWGCAFRQVC	624						
RESULT 66									
T11566									
envelope glycoprotein - simian immunodeficiency virus SIVsm (strain E543)									
C;Species: simian immunodeficiency virus SIVsm									
A;Variety: strain E543									
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000									

C;Accession: T11566

R;Hirsch, V.M.; Adger-Johnson, D.; Cambell, B.; Goldstein, S.; Brown, C.; Elkins, W.R.; J. Virol. 71, 1608-1620, 1997

A;Title: A molecularly cloned, pathogenic, neutralization-resistant simian immunodeficiency virus

A;Reference number: Z17285; MUID:97151152; PMID:8995688

A;Accession: T11566

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-887 <HIR>

A;Cross-references: EMBL:U72748; NID:g1695908; PIDN:AAC56565.1; PID:g1695916

C;Genetics:

A;Gene: env

C;Superfamily: type E retrovirus env polyprotein

C;Keywords: AIDS; immunodeficiency

Query Match 59.7%; Score 83; DB 2; Length 887;

Best Local Similarity 50.0%; Pred. No. 0.0002;

Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGIWGCSGKLIC 26

Db 600 RVTAIEKYLKDQAQLNSWGCAFRQVC 625

RESULT 67

C46356

env polyprotein - simian immunodeficiency virus SIVagm (type 3)

C;Species: simian immunodeficiency virus SIVagm

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 26-Aug-1999

C;Accession: C46356; G36860

R;Baier, M.; Garber, C.; Mueller, C.; Cichutek, K.; Kurth, R. Virology 176, 216-221, 1990

A;Title: Complete nucleotide sequence of a simian immunodeficiency virus from African green monkey

A;Reference number: A46356; MUID:90232731; PMID:2158689

A;Accession: C46356

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-877 <BA2>

A;Cross-references: GB:M30931; NID:g334400; PIDN:AAA91919.1; PID:g334407

C;Superfamily: type E retrovirus env polyprotein

C;Keywords: polyprotein; transmembrane protein

Query Match 59.0%; Score 82; DB 2; Length 877;

Best Local Similarity 50.0%; Pred. No. 0.00028;

Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGIWGCSGKLIC 26

Db 610 RVTALEKYLEQARLNAWGCAWKQVC 635

RESULT 68

VCLJG4

env polyprotein - simian immunodeficiency virus (African green monkey isolate)

C;Species: simian immunodeficiency virus, SIV

C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 24-Oct-1997

C;Accession: G30045

R;Fukasawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Miki, K.; Kitamura, T. Nature 333, 457-461, 1988

A;Title: Sequence of simian immunodeficiency virus from African green monkey, a new member of the genus Simiavirus

A;Reference number: A30045; MUID:88232906; PMID:3374586

A;Accession: G30045

A;Molecule type: DNA

A;Residues: 1-864 <FUK>

A;Cross-references: EMBL:X07805

C;Genetics:

A;Gene: env

C;Superfamily: type E retrovirus env polyprotein

C;Keywords: AIDS; capsid protein; coat protein; immunodeficiency; polyprotein; transmembrane protein

Query Match 58.3%; Score 81; DB 1; Length 864;

Best Local Similarity 50.0%; Pred. No. 0.0004;

Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;



```
A;Accession: C26262
A:Molecule type: DNA
A;Residues: 1-858 <GUY>
A;Cross-references: GB:M15390; NID:g1332361; PIDN:AAB00770.1; PID:g325749
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-858/Product: env polyprotein #status predicted <MAT>
F;18-501/Product: exterior membrane glycoprotein #status predicted <EXT>
F;502-858/Product: transmembrane glycoprotein #status predicted <TM>
F;34,67,76,119,120,151,166,179,192,193,196,206,238,241,248,272,278,289,300,367,371,400,4
```

Search completed: May 3, 2004, 06:22:48  
Job time : 39 secs